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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 4.60064 seconds  
(without alignments)  
146.032 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_222\_230  
Perfect score: 49  
Sequence: 1 LQYALFPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	107	3	US-08-483-749A-26
2	49	100.0	243	1	US-08-133-804-6
3	49	100.0	243	1	US-08-461-838-6
4	49	100.0	243	2	US-08-461-386-6
5	49	100.0	243	2	US-08-356-786-4
6	49	100.0	534	2	US-08-356-786-10
7	36	73.5	92	2	US-08-273-146-47
8	36	73.5	107	4	US-09-648-067A-10
9	36	73.5	107	4	US-09-648-067A-12
10	36	73.5	215	2	US-08-737-129A-8
11	36	73.5	355	3	US-08-875-811-41
12	36	73.5	355	3	US-08-875-811-49
13	36	73.5	355	3	US-08-875-811-64
14	36	73.5	358	3	US-08-875-811-45
15	36	73.5	358	3	US-08-875-811-51
16	36	73.5	360	3	US-08-875-811-47
17	36	73.5	379	3	US-08-875-811-43
18	35	71.4	92	2	US-08-273-146-45
19	35	71.4	92	2	US-08-273-146-53
20	35	71.4	107	3	US-08-483-749A-12
21	35	71.4	145	3	US-09-096-244-2
22	35	71.4	490	4	US-09-270-767-42437
23	34	69.4	107	1	US-07-634-278-50
24	34	69.4	107	1	US-07-634-278-51
25	34	69.4	107	1	US-08-477-728-50
26	34	69.4	107	1	US-08-477-728-51
27	34	69.4	107	1	US-08-474-040-50

28	34	69.4	107	1	US-08-474-040-51	Sequence 51, Appl
29	34	69.4	107	1	US-08-487-200-50	Sequence 50, Appl
30	34	69.4	107	1	US-08-487-200-51	Sequence 51, Appl
31	34	69.4	107	3	US-08-484-537-50	Sequence 50, Appl
32	34	69.4	107	3	US-08-484-537-51	Sequence 51, Appl
33	34	69.4	165	4	US-09-248-796A-22117	Sequence 22117, A
34	34	69.4	313	4	US-09-270-767-42252	Sequence 42252, A
35	34	69.4	322	4	US-09-328-352-5739	Sequence 5739, Ap
36	33	67.3	106	1	US-08-202-047-26	Sequence 26, Appl
37	33	67.3	106	3	US-08-964-690-26	Sequence 26, Appl
38	33	67.3	156	4	US-09-902-540-14530	Sequence 14530, A
39	33	67.3	345	4	US-09-134-000C-5010	Sequence 5010, Ap
40	33	67.3	388	4	US-09-560-761B-20	Sequence 20, Appl
41	32	65.3	95	2	US-08-713-939A-72	Sequence 72, Appl
42	32	65.3	95	3	US-09-036-579-72	Sequence 72, Appl
43	32	65.3	95	3	US-09-550-374-72	Sequence 72, Appl
44	32	65.3	95	4	US-09-943-906-72	Sequence 72, Appl
45	32	65.3	107	2	US-08-290-592E-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1  
US-08-483-749A-26  
Sequence 26, Application US/08483749A  
Patent No. 6094561  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESSES:  
ADDRESS: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
CITY: EMERYVILLE  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,749A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVERIDE, PAUL B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0508.008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-749A-26  
Query Match 100.0%; Score 49; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LQYALFPT 9  
|||  
Db 89 LQYALFPT 97  
RESULT 2

US-08-133-804-6  
Sequence 6, Application US/08133804  
Patent No. 5534254  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Houston, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
TITLE OF INVENTION: Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/133,804  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-133-804-6

Query Match 100.0%; Score 49; DB 1; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYAIFFPT 9  
DB 222 LOYAIFFPT 230

RESULT 3  
US-08-461-838-6  
Sequence 6, Application US/08461838  
Patent No. 5753204  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
TITLE OF INVENTION: Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,838  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-461-838-6

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,838  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-461-838-6

Query Match 100.0%; Score 49; DB 1; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYAIFFPT 9  
DB 222 LOYAIFFPT 230

RESULT 4  
US-08-461-386-6  
Sequence 6, Application US/08461386  
Patent No. 5837846  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
TITLE OF INVENTION: Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,386  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-461-386-6

Query Match 100.0%; Score 49; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOYALFPHYT 9  
|||  
Db 222 LOYALFPHYT 230

RESULT 5  
US-08-356-786-4

; Sequence 4, Application US/08356786  
; Patent No. 5877305

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Oppermann, Hermann

; APPLICANT: Houston, L. L.

; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edmund R. Pltcher, Testa, Hurwitz, & Thibault

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/356,786

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/831,967

; FILING DATE: 06-FEB-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Pltcher, Edmund R.

; REGISTRATION NUMBER: 27,829

; REFERENCE/DOCKET NUMBER: CRP-053

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 248-7000

; TELEFAX: (617) 248-7100

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 243 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-356-786-4

Query Match 100.0%; Score 49; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOYALFPHYT 9  
|||  
Db 222 LOYALFPHYT 230

RESULT 6

US-08-356-786-10

; Sequence 10, Application US/08356786  
; Patent No. 5877305

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Oppermann, Hermann

; APPLICANT: Houston, L. L.

; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edmund R. Pltcher, Testa, Hurwitz, & Thibault

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/356,786

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/831,967

; FILING DATE: 06-FEB-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Pltcher, Edmund R.

; REGISTRATION NUMBER: 27,829

; REFERENCE/DOCKET NUMBER: CRP-053

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 248-7000

; TELEFAX: (617) 248-7100

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 534 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-356-786-10

Query Match 100.0%; Score 49; DB 2; Length 534;  
Best Local Similarity 100.0%; Pred. No. 0.71;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOYALFPHYT 9  
|||  
Db 513 LOYALFPHYT 521

RESULT 7

US-08-273-146-47

; Sequence 47, Application US/08273146  
; Patent No. 5853865

; GENERAL INFORMATION:

; APPLICANT: Smith, Rodger

; APPLICANT: McCafferty, John

; APPLICANT: Chiswell, David

; APPLICANT: Darsley, Michael J.

; APPLICANT: Fitzgerald, Kevin

; APPLICANT: Kenten, John H.

; APPLICANT: Martin, Mark T.

; APPLICANT: Titmas, Richard C.

; TITLE OF INVENTION: The Isolation and Production of

; NUMBER OF SEQUENCES: 71

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: IGEN, Inc.

; STREET: 1530 East Jefferson St.

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20852

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/273,146  
FILING DATE: 14-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ryan, John W.  
REGISTRATION NUMBER: 33,771  
REFERENCE/DOCKET NUMBER: 09000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-984-8000  
TELEFAX: 301-230-0158  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-273-146-47

Query Match 73.5%; Score 36; DB 2; Length 92;  
Best Local Similarity 77.8%; Pred. No. 25;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYAFPPYT 9  
|||:||||  
Db 81 LOYDERPPYT 89

RESULT 8  
US-09-648-067A-10  
Sequence 10, Application US/09648067A  
Patent No. 6627196  
GENERAL INFORMATION:  
APPLICANT: Baughman, Sharon A.  
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies  
FILE REFERENCE: P1775R1  
CURRENT APPLICATION NUMBER: US/09/648,067A  
CURRENT FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: US 60/151,018  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: US 60/213,822  
PRIOR FILING DATE: 2000-06-23  
NUMBER OF SEQ ID NOS: 15  
SEQ ID NO 10  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Mus Musculus  
US-09-648-067A-10

Query Match 73.5%; Score 36; DB 4; Length 107;  
Best Local Similarity 75.0%; Pred. No. 28;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAFPPYT 9  
|||:||||  
Db 90 QYIYPPYT 97

RESULT 9  
US-09-648-067A-12  
Sequence 12, Application US/09648067A  
Patent No. 6627196  
GENERAL INFORMATION:  
APPLICANT: Baughman, Sharon A.  
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies  
FILE REFERENCE: P1775R1  
CURRENT APPLICATION NUMBER: US/09/648,067A  
CURRENT FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: US 60/151,018

PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: US 60/213,822  
PRIOR FILING DATE: 2000-06-23  
NUMBER OF SEQ ID NOS: 15  
SEQ ID NO 12  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: humanized VL sequence  
US-09-648-067A-12

Query Match 73.5%; Score 36; DB 4; Length 107;  
Best Local Similarity 75.0%; Pred. No. 28;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAFPPYT 9  
|||:||||  
Db 90 QYIYPPYT 97

RESULT 10  
US-08-737-129A-8  
Sequence 8, Application US/08737129A  
Patent No. 5885816  
GENERAL INFORMATION:  
APPLICANT: Ikuo FUJII et al.  
TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY  
HYDROLYSING AMINO ACID ESTER DERIVATIVES  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Menderoth, Lind & Penack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/737,129A  
FILING DATE: No. 5885816ember 15, 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-737-129A-8

Query Match 73.5%; Score 36; DB 2; Length 215;  
Best Local Similarity 77.8%; Pred. No. 54;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYAFPPYT 9  
|||:||||  
Db 89 LOYDERPPYT 97



RESULT 11  
US-08-875-811-41  
; Sequence 41, Application US/08875811  
; Patent No. 6045793  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Bogue, Lluís  
; APPLICANT: Mlodawer, Alexander  
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/875,811  
; FILING DATE: 19-FEB-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/02588  
; FILING DATE: 19-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,800  
; FILING DATE: 21-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Faris, Susan K.  
; REGISTRATION NUMBER: 41,739  
; REFERENCE/DOCKET NUMBER: 015280-244100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 355 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-875-811-41

Query Match 73.5%; Score 36; DB 3; Length 355;  
Best Local Similarity 77.8%; Pred. No. 87;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1 LOYALPPT 9  
DB 89 LOYDEPPT 97

RESULT 12  
US-08-875-811-49  
; Sequence 49, Application US/08875811  
; Patent No. 6045793  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Bogue, Lluís  
; APPLICANT: Mlodawer, Alexander  
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/875,811  
; FILING DATE: 19-FEB-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/02588  
; FILING DATE: 19-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,800  
; FILING DATE: 21-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Faris, Susan K.  
; REGISTRATION NUMBER: 41,739  
; REFERENCE/DOCKET NUMBER: 015280-244100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 355 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-875-811-49

Query Match 73.5%; Score 36; DB 3; Length 355;  
Best Local Similarity 77.8%; Pred. No. 87;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1 LOYALPPT 9  
DB 89 LOYDEPPT 97

RESULT 13  
US-08-875-811-64  
; Sequence 64, Application US/08875811  
; Patent No. 6045793  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Bogue, Lluís  
; APPLICANT: Mlodawer, Alexander  
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/875,811  
; FILING DATE: 19-FEB-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/02588  
; FILING DATE: 19-FEB-1997

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Faris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..355  
OTHER INFORMATION: /note= "B6FB[Mec-(-1)]SerOnc"  
US-08-875-811-64

Query Match  
Best Local Similarity 77.8%; Score 36; DB 3; Length 355;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQYAFPYT 9  
DB 89 LQYDEFPYT 97

RESULT 14  
US-08-875-811-45  
Sequence 45, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Luis  
APPLICANT: Mlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..355  
OTHER INFORMATION: /note= "B6FB[Mec-(-1)]SerOnc"  
US-08-875-811-64

Query Match  
Best Local Similarity 77.8%; Score 36; DB 3; Length 355;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQYAFPYT 9  
DB 89 LQYDEFPYT 97

RESULT 15  
US-08-875-811-51  
Sequence 51, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Luis  
APPLICANT: Mlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..358  
OTHER INFORMATION: /note= "B6FB[Mec-(-1)]SerOnc"  
US-08-875-811-51

Query Match  
Best Local Similarity 77.8%; Score 36; DB 3; Length 358;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQYAFPYT 9  
DB 207 LQYDEFPYT 215

SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-45

Query Match  
Best Local Similarity 77.8%; Score 36; DB 3; Length 358;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQYAFPYT 9  
DB 207 LQYDEFPYT 215

RESULT 15  
US-08-875-811-51  
Sequence 51, Application US/08875811  
Patent No. 6045793

GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Luis  
APPLICANT: Mlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..358  
OTHER INFORMATION: /note= "B6FB[Mec-(-1)]SerOnc"  
US-08-875-811-51

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..358  
OTHER INFORMATION: /note= "B6FB[Mec-(-1)]SerOnc"  
US-08-875-811-51

Query Match  
Best Local Similarity 77.8%; Score 36; DB 3; Length 358;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQYAFPYT 9  
DB 207 LQYDEFPYT 215

Tue Apr 5 08:00:43 2005

us-09-887-853-6\_copy\_222\_230.ra1

Page 7

Search completed: April 4, 2005, 16:00:52  
Job time : 4.60064 secs

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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 3.57827 Seconds

(without alignments)  
146.032 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_183\_189

Perfect score: 31

Sequence: 1 ATSSUDS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCITUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	92	2	US-08-273-146-45
2	31	100.0	92	2	US-08-273-146-53
3	31	100.0	107	3	US-08-483-748A-26
4	31	100.0	108	4	US-09-726-218A-267
5	31	100.0	109	1	US-08-466-886-27
6	31	100.0	109	2	US-08-713-939A-74
7	31	100.0	109	3	US-08-469-617-27
8	31	100.0	109	3	US-09-036-579-74
9	31	100.0	109	3	US-09-550-374-74
10	31	100.0	109	4	US-09-943-906-74
11	31	100.0	109	4	US-08-469-630-27
12	31	100.0	112	4	US-09-627-218B-1
13	31	100.0	243	1	US-08-133-804-6
14	31	100.0	243	1	US-08-461-838-6
15	31	100.0	243	2	US-08-461-386-6
16	31	100.0	243	2	US-08-356-786-4
17	31	100.0	534	2	US-08-356-786-10
18	31	100.0	694	2	US-08-895-522-3
19	31	100.0	694	3	US-09-195-391-3
20	31	100.0	747	2	US-08-895-522-1
21	31	100.0	747	3	US-09-195-391-1
22	28	90.3	109	1	US-08-466-886-26
23	28	90.3	109	3	US-08-469-617-26
24	28	90.3	109	4	US-08-469-630-26
25	28	90.3	111	4	US-09-248-796A-20768
26	28	90.3	313	4	US-09-134-000C-5794
27	28	90.3	439	4	US-09-902-540-11372

28	28	90.3	614	4	US-09-540-236-2858	Sequence 2858, Appl
29	28	90.3	617	4	US-09-328-352-6700	Sequence 6700, Appl
30	28	90.3	624	4	US-09-252-991A-21625	Sequence 21625, A
31	28	90.3	744	4	US-09-248-796A-20773	Sequence 20773, A
32	28	90.3	1307	1	US-08-395-246C-2	Sequence 2, Appl1
33	28	90.3	1334	2	US-08-996-545-2	Sequence 2, Appl1
34	28	90.3	1334	3	US-09-328-320-2	Sequence 2, Appl1
35	28	90.3	1334	4	US-09-758-828-2	Sequence 2, Appl1
36	28	90.3	1349	2	US-08-612-734B-2	Sequence 2, Appl1
37	28	90.3	1402	4	US-09-711-619-9	Sequence 9, Appl1
38	28	90.3	1408	1	US-08-612-521-2	Sequence 2, Appl1
39	27	87.1	105	3	US-08-881-189B-13	Sequence 13, Appl
40	27	87.1	107	2	US-08-888-366-14	Sequence 14, Appl
41	27	87.1	107	2	US-08-888-366-20	Sequence 20, Appl
42	27	87.1	107	2	US-08-888-366-26	Sequence 26, Appl
43	27	87.1	108	4	US-09-270-767-35025	Sequence 35025, A
44	27	87.1	108	4	US-09-270-767-50242	Sequence 50242, A
45	27	87.1	243	4	US-09-134-000C-5004	Sequence 5004, Appl

#### ALIGNMENTS

RESULT 1  
US-08-273-146-45  
Sequence 45, Application US/08273146  
Patent No. 5855865  
GENERAL INFORMATION:  
APPLICANT: Smith, Rodger  
APPLICANT: McCafferty, John  
APPLICANT: Chiswell, David  
APPLICANT: Darzley, Michael J.  
APPLICANT: Fitzgerald, Kevin  
APPLICANT: Kanten, John H.  
APPLICANT: Martin, Mark T.  
APPLICANT: Titmas, Richard C.  
APPLICANT: Williams, Richard O.  
TITLE OF INVENTION: The isolation and production of  
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IGEN, Inc.  
STREET: 1530 East Jefferson St.  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20852  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/273,146  
FILING DATE: 14-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ryan, John W.  
REGISTRATION NUMBER: 33,771  
REFERENCE/DOCKET NUMBER: 09000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-984-8000  
TELEFAX: 301-230-0158  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-273-146-45  
Query Match 100.0%; Score 31; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 6.9;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7  
Db 42 ATSSIDS 48

## RESULT 2

US-08-273-146-53  
; Sequence 53, Application US/08273146  
; Patent No. 5855885  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Rodger  
; APPLICANT: McCafferty, John  
; APPLICANT: Chiswell, David  
; APPLICANT: Darsley, Michael J.  
; APPLICANT: Fitzgerald, Kevin  
; APPLICANT: Kerten, John H.  
; APPLICANT: Martin, Mark T.  
; APPLICANT: Tlmas, Richard C.  
; APPLICANT: Williams, Richard O.  
; TITLE OF INVENTION: The Isolation and Production of  
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IGEN, Inc.  
; STREET: 1530 East Jefferson St.  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20852  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/273,146  
; FILING DATE: 14-JUL-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ryan, John W.  
; REGISTRATION NUMBER: 33,771  
; REFERENCE/DOCKET NUMBER: 09000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-984-8000  
; TELEFAX: 301-230-0158  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 92 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-273-146-53

Query Match 100.0%; Score 31; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 6.9; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7  
Db 42 ATSSIDS 48

RESULT 3  
US-08-483-749A-26  
; Sequence 26, Application US/08483749A  
; Patent No. 6054561  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
; NUMBER OF SEQUENCES: 33

## CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
CITY: EMERYVILLE  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,749A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVERIDE, PAUL B.  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0508,008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-749A-26

Query Match 100.0%; Score 31; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 8.2; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7  
Db 50 ATSSIDS 56

RESULT 4  
US-09-726-219A-267  
; Sequence 267, Application US/09726219A  
; Patent No. 6806079  
; GENERAL INFORMATION:  
; APPLICANT: Cambridge Antibody Technology  
; APPLICANT: Cambridge Antibody Technology Limited  
; APPLICANT: Medical Research Council  
; APPLICANT: McCafferty, John  
; APPLICANT: Pope, Anthony  
; APPLICANT: Johnson, Kevin  
; APPLICANT: Hoogenboom, Hendricus  
; APPLICANT: Griffiths, Andrew  
; APPLICANT: Jackson, Ronald  
; APPLICANT: Holliger, Kasper  
; APPLICANT: Marks, James  
; APPLICANT: Clackson, Timothy  
; APPLICANT: Chiswell, David  
; APPLICANT: Winter, Gregory  
; APPLICANT: Bonert, Timothy  
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
; FILE REFERENCE: 213839-00013  
; CURRENT APPLICATION NUMBER: US/09/726,219A  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: GB 9015198.6  
; PRIOR FILING DATE: 1990-07-10  
; PRIOR APPLICATION NUMBER: GB 9022845.3  
; PRIOR FILING DATE: 1990-10-19  
; PRIOR APPLICATION NUMBER: GB 9022845.3  
; PRIOR FILING DATE: 1990-10-19  
; PRIOR APPLICATION NUMBER: GB 9024503.6  
; PRIOR FILING DATE: 1990-11-12  
; PRIOR APPLICATION NUMBER: GB 9104744.9

PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-08  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 267  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: light chain from clone M1F  
US-09-726-219A-267

Query Match 100.0%; Score 31; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 8.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7  
Db 50 ATSSIDS 56

RESULT 5  
US-08-466-886-27  
Sequence 27, Application US/08466886  
Patent No. 5776677  
GENERAL INFORMATION:  
APPLICANT: Teul, Lap-Chee  
APPLICANT: Riordan, John R.  
APPLICANT: Rommens, Johanna M.  
APPLICANT: Kerem, Bat-Sheva  
APPLICANT: Collins, Francis S.  
APPLICANT: Iannuzzi, Michael C.  
APPLICANT: Drumm, Mitchell L.  
TITLE OF INVENTION: Cyclic Fibrosis Gene  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,886  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 1329.0010006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2500  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide

US-08-466-886-27

Query Match 100.0%; Score 31; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7  
Db 99 ATSSIDS 105

RESULT 6  
US-08-713-939A-74  
Sequence 74, Application US/08713939A  
Patent No. 5846533  
GENERAL INFORMATION:  
APPLICANT: Pusiner, Stanley B.  
APPLICANT: Williamson, R. Anthony  
APPLICANT: Burton, Dennis R.  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PRP  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/713,939A  
FILING DATE: 13-SEP-1996  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bozicevic, Karl  
REGISTRATION NUMBER: 28,807  
REFERENCE/DOCKET NUMBER: 06510/059001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-5277  
TELEFAX: 415-854-0875  
TELEX:  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-713-939A-74

Query Match 100.0%; Score 31; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7  
Db 50 ATSSIDS 56

RESULT 7  
US-08-469-617-27  
Sequence 27, Application US/08469617  
Patent No. 6201107  
GENERAL INFORMATION:  
APPLICANT: Teul, Lap-Chee  
APPLICANT: Riordan, John R.

APPLICANT: Rommens, Johanna M.  
APPLICANT: Kerem, Bat-Sheva  
APPLICANT: Collins, Francis S.  
APPLICANT: Iannuzzi, Michael C.  
APPLICANT: Drumm, Mitchell L.  
APPLICANT: Buckwald, Manuel  
TITLE OF INVENTION: Cystic Fibrosis Gene  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,617  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 1329.0010008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-469-617-27  
Query Match 100.0%; Score 31; DB 3; Length 109;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ATSSIDS 7  
Db 99 ATSSIDS 105  
RESULT 8  
US-09-036-579-74  
Sequence 74, Application US/09036579  
Patent No. 6290954  
GENERAL INFORMATION:  
APPLICANT: Prusiner, Stanley B.  
APPLICANT: Williamson, R. Anthony  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/036,579

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/713,939  
FILING DATE: 13-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bozicevic, Karl  
REGISTRATION NUMBER: 28,807  
REFERENCE/DOCKET NUMBER: 06510/059001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-5277  
TELEFAX: 415-854-0875  
TELEX:  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-036-579-74  
Query Match 100.0%; Score 31; DB 3; Length 109;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ATSSIDS 7  
Db 50 ATSSIDS 56

RESULT 9  
US-09-550-374-74  
Sequence 74, Application US/09550374  
Patent No. 6372214  
GENERAL INFORMATION:  
APPLICANT: Prusiner, Stanley B.  
APPLICANT: Williamson, R. Anthony  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/550,374  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/036,579  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bozicevic, Karl  
REGISTRATION NUMBER: 28,807  
REFERENCE/DOCKET NUMBER: 06510/059001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-5277  
TELEFAX: 415-854-0875  
TELEX:  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: single



TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-550-374-74

Query Match  
Best Local Similarity 100.0%; Score 31; DB 3; Length 109;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
Db 50 ATSSIDS 56

RESULT 10  
US-09-943-906-74  
Sequence 74, Application US/09943906  
Patent No. 6562341  
GENERAL INFORMATION:  
APPLICANT: Prusiner, Stanley B.  
Williamson, R. Anthony  
Burton, Dennis R.  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/943,906  
FILING DATE: 30-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/550,374  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Bozicevic, Karl  
REGISTRATION NUMBER: 28,807  
REFERENCE/DOCKET NUMBER: 06510/059001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-5277  
TELEFAX: 415-854-0875  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 74:  
US-09-943-906-74

Query Match  
Best Local Similarity 100.0%; Score 31; DB 4; Length 109;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
Db 50 ATSSIDS 56

RESULT 11  
US-08-469-630-27  
Sequence 27, Application US/08469630  
Patent No. 6730777

GENERAL INFORMATION:  
APPLICANT: Tsui, Lap-Chee  
APPLICANT: Riordan, John R.  
APPLICANT: Rommens, Johanna M.  
APPLICANT: Kerem, Bat-Sheva  
APPLICANT: Collins, Francis S.  
APPLICANT: Iannuzzi, Michael C.  
APPLICANT: Drumm, Mitchell L.  
APPLICANT: Buckwald, Manuel  
TITLE OF INVENTION: Cyclic Fibrosis Gene  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,630  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 1329.0010005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-469-630-27

Query Match  
Best Local Similarity 100.0%; Score 31; DB 4; Length 109;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
Db 99 ATSSIDS 105

RESULT 12  
US-09-627-218B-1  
Sequence 1, Application US/09627218B  
Patent No. 6537548  
GENERAL INFORMATION:  
APPLICANT: Prusiner, Stanley  
APPLICANT: Safar, Jiri  
APPLICANT: Williamson, Anthony  
APPLICANT: Burton, Dennis  
TITLE OF INVENTION: Antibodies Specific for Ungulate PrP  
FILE REFERENCE: UCAL-194  
CURRENT APPLICATION NUMBER: US/09/627,218B  
CURRENT FILING DATE: 2000-07-27  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 112  
TYPE: PrP  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthesized peptide

US-09-627-218B-1

Query Match 100.0%; Score 31; DB 4; Length 112;  
Best Local Similarity 100.0%; Pred. No. 8.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
DB 50 ATSSIDS 56

RESULT 13

US-08-133-804-6  
; Sequence 6, Application US/08133804  
; Patent No. 5534254  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Proteins For  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Testa, Hurwitz & Thibault/Patent Department  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/133,804  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kelley, Robin D.  
; REGISTRATION NUMBER: 34,637  
; REFERENCE/DOCKET NUMBER: 2054/22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-248-7477  
; TELEFAX: 617-248-7100  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 243 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-133-804-6

Query Match 100.0%; Score 31; DB 1; Length 243;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
DB 183 ATSSIDS 189

RESULT 14  
US-08-461-838-6  
; Sequence 6, Application US/08461838  
; Patent No. 5753204  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Proteins For

TITLE OF INVENTION: Imaging

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSER: Testa, Hurwitz &amp; Thibault/Patent Department

STREET: Exchange Place, 53 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,838

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Kelley, Robin D.

REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: 2054/22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7477

TELEFAX: 617-248-7100

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 243 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-461-838-6

Query Match 100.0%; Score 31; DB 1; Length 243;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
DB 183 ATSSIDS 189

RESULT 15  
US-08-461-386-6  
; Sequence 6, Application US/08461386  
; Patent No. 5837846  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Proteins For  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Testa, Hurwitz & Thibault/Patent Department  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,386  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kelley, Robin D.  
; REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: 2054/22  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-248-7477  
 TELEFAX: 617-248-7100  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 243 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-461-386-6

Query Match 100.0%; Score 31; DB 2; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7  
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 DB 183 ATSSIDS 189

Search completed: April 4, 2005, 16:00:52  
 Job time : 4.57827 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 5.623 Seconds  
(without alignments)

146.032 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_157\_167

Perfect score: 53

Sequence: 1 RASODIGNSLT 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/pdata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/pdata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/pdata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/pdata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/pdata/1/1aa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/pdata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	107	3	US-08-483-749A-26
2	53	100.0	243	1	US-08-133-804-6
3	53	100.0	243	1	US-08-461-838-6
4	53	100.0	243	2	US-08-461-386-6
5	53	100.0	243	2	US-08-356-786-4
6	53	100.0	534	2	US-08-356-786-10
7	45	84.9	112	4	US-09-627-218B-1
8	43	81.1	92	2	US-08-273-146-45
9	43	81.1	92	2	US-08-273-146-53
10	43	81.1	107	2	US-08-888-366-14
11	43	81.1	107	2	US-08-888-366-20
12	43	81.1	107	2	US-08-888-366-26
13	43	81.1	108	4	US-09-726-219A-267
14	43	81.1	109	2	US-08-713-939A-74
15	43	81.1	109	3	US-09-036-579-74
16	43	81.1	109	3	US-09-550-374-74
17	43	81.1	109	4	US-09-943-906-74
18	42	79.2	11	4	US-09-155-106-4
19	42	79.2	108	4	US-09-155-106-22
20	42	79.2	108	4	US-09-155-106-23
21	42	79.2	108	4	US-09-155-106-24
22	42	79.2	108	4	US-09-155-106-28
23	42	79.2	108	4	US-09-155-106-30
24	39	73.6	11	1	US-07-942-245-497
25	39	73.6	31	3	US-08-525-539A-3
26	39	73.6	95	2	US-08-713-939A-72
27	39	73.6	95	3	US-09-036-579-72

28	39	73.6	95	3	US-09-550-374-72	Sequence 72, Appl
29	39	73.6	95	4	US-09-943-906-72	Sequence 72, Appl
30	39	73.6	107	1	US-08-436-463-20	Sequence 20, Appl
31	39	73.6	107	1	US-08-107-669D-1	Sequence 1, Appl
32	39	73.6	107	1	US-08-472-768A-1	Sequence 1, Appl
33	39	73.6	107	2	US-08-477-531B-1	Sequence 1, Appl
34	39	73.6	107	2	US-08-082-842A-1	Sequence 1, Appl
35	39	73.6	108	2	US-08-378-939-26	Sequence 26, Appl
36	39	73.6	108	4	US-09-232-230-27	Sequence 27, Appl
37	39	73.6	109	1	US-07-942-245-4	Sequence 4, Appl
38	39	73.6	109	2	US-08-713-939A-73	Sequence 73, Appl
39	39	73.6	109	3	US-09-036-579-73	Sequence 73, Appl
40	39	73.6	109	3	US-09-550-374-73	Sequence 73, Appl
41	39	73.6	109	4	US-09-943-906-73	Sequence 73, Appl
42	38	71.7	11	4	US-09-192-854-170	Sequence 170, Appl
43	38	71.7	106	4	US-08-635-109-8	Sequence 8, Appl
44	38	71.7	106	4	US-08-844-215-11	Sequence 11, Appl
45	37	69.8	96	4	US-09-472-087-99	Sequence 99, Appl

## ALIGNMENTS

RESULT 1  
US-08-483-749A-26  
Sequence 26, Application US/08483749A  
Patent No. 6054561  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
CITY: EMERYVILLE  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,749A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVERIDE, PAUL B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0508, 008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-749A-26  
Query Match 100.0%; Score 53; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RASODIGNSLT 11  
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DB 24 RASODIGNSLT 34  
RESULT 2

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US-08-133-804-6
/ Sequence 6, Application US/08133804
/ Patent No. 5534254
/ GENERAL INFORMATION:
/ APPLICANT: Huston, James S.
/ APPLICANT: Oppermann, Hermann
/ APPLICANT: Houston, L. L.
/ APPLICANT: Ring, David B.
/ TITLE OF INVENTION: Biosynthetic Binding Proteins For
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Testa, Hurwitz & Thibault/Patent Department
/ STREET: Exchange Place, 53 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/133,804
/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kelley, Robin D.
/ REGISTRATION NUMBER: 34,637
/ REFERENCE/DOCKET NUMBER: 2054/22
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-248-7477
/ TELEFAX: 617-248-7100
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 243 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-133-804-6

Query Match      100.0%; Score 53; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQDIGNSLT 11
Db      157 RASQDIGNSLT 167

RESULT 3
US-08-461-838-6
/ Sequence 6, Application US/08461838
/ Patent No. 5753204
/ GENERAL INFORMATION:
/ APPLICANT: Huston, James S.
/ APPLICANT: Oppermann, Hermann
/ APPLICANT: Houston, L. L.
/ APPLICANT: Ring, David B.
/ TITLE OF INVENTION: Biosynthetic Binding Proteins For
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Testa, Hurwitz & Thibault/Patent Department
/ STREET: Exchange Place, 53 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/461,386
/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kelley, Robin D.
/ REGISTRATION NUMBER: 34,637
/ REFERENCE/DOCKET NUMBER: 2054/22
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-248-7477
/ TELEFAX: 617-248-7100
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 243 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-461-386-6

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/461,838
/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kelley, Robin D.
/ REGISTRATION NUMBER: 34,637
/ REFERENCE/DOCKET NUMBER: 2054/22
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-248-7477
/ TELEFAX: 617-248-7100
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 243 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-461-838-6

Query Match      100.0%; Score 53; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQDIGNSLT 11
Db      157 RASQDIGNSLT 167

RESULT 4
US-08-461-386-6
/ Sequence 6, Application US/08461386
/ Patent No. 5837846
/ GENERAL INFORMATION:
/ APPLICANT: Huston, James S.
/ APPLICANT: Oppermann, Hermann
/ APPLICANT: Houston, L. L.
/ APPLICANT: Ring, David B.
/ TITLE OF INVENTION: Biosynthetic Binding Proteins For
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Testa, Hurwitz & Thibault/Patent Department
/ STREET: Exchange Place, 53 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/461,386
/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kelley, Robin D.
/ REGISTRATION NUMBER: 34,637
/ REFERENCE/DOCKET NUMBER: 2054/22
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-248-7477
/ TELEFAX: 617-248-7100
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 243 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-461-386-6

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Query Match 100.0%; Score 53; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.0074;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11  
|||||  
Db 157 RASODIGNSLT 167

RESULT 5  
US-08-356-786-4  
; Sequence 4, Application US/08356786  
; Patent No. 5877305  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
; TITLE OF INVENTION: Marker  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/356,786  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/831,967  
; FILING DATE: 06-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pitcher, Edmund R.  
; REGISTRATION NUMBER: 27,829  
; REFERENCE/DOCKET NUMBER: CRP-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7100  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 243 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-356-786-4

Query Match 100.0%; Score 53; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.0074;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11  
|||||  
Db 157 RASODIGNSLT 167

RESULT 6  
US-08-356-786-10  
; Sequence 10, Application US/08356786  
; Patent No. 5877305  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
; TITLE OF INVENTION: Marker  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/356,786  
; FILING DATE:  
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/831,967  
; FILING DATE: 06-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pitcher, Edmund R.  
; REGISTRATION NUMBER: 27,829  
; REFERENCE/DOCKET NUMBER: CRP-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7100  
; TELEFAX: (617) 248-7100

; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 534 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-356-786-10

Query Match 100.0%; Score 53; DB 2; Length 534;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11  
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Db 448 RASODIGNSLT 458

RESULT 7  
US-09-627-218B-1  
; Sequence 1, Application US/09627218B  
; Patent No. 6537548  
; GENERAL INFORMATION:  
; APPLICANT: Prusiner, Stanley  
; APPLICANT: Safar, Jiri  
; APPLICANT: Williamson, Anthony  
; APPLICANT: Burton, Dennis  
; TITLE OF INVENTION: Antibodies Specific for Ungulate PrP  
; FILE REFERENCE: UCAL-194  
; CURRENT APPLICATION NUMBER: US/09/627,218B  
; CURRENT FILING DATE: 2000-07-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthesized peptide  
US-09-627-218B-1

Query Match 84.9%; Score 45; DB 4; Length 112;  
Best Local Similarity 90.0%; Pred. No. 0.13;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASODIGNSL 10  
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Db 24 RASODIGNSL 33

RESULT 8  
US-08-273-146-45  
; Sequence 45, Application US/08273146  
; Patent No. 5855885  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Rodger  
; APPLICANT: McCallister, John  
; APPLICANT: Chiswell, David  
; APPLICANT: Darsley, Michael J.  
; APPLICANT: Fitzgerald, Kevin  
; APPLICANT: Kerten, John H.  
; APPLICANT: Martin, Mark T.  
; APPLICANT: Williams, Richard C.  
; TITLE OF INVENTION: The Isolation and Production of  
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IGEN, Inc.  
; STREET: 1530 East Jefferson St.  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20852  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/273,146  
; FILING DATE: 14-JUL-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ryan, John W.  
; REGISTRATION NUMBER: 33,771  
; REFERENCE/DOCKET NUMBER: 09000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-984-8000  
; TELEFAX: 301-230-0158  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 92 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-273-146-45

Query Match 81.1%; Score 43; DB 2; Length 92;  
Best Local Similarity 90.0%; Pred. No. 0.26;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASODIGNSL 10  
|||:|  
Db 16 RASODIGNSL 25

RESULT 9  
US-08-273-146-53  
; Sequence 53, Application US/08273146  
; Patent No. 5855885  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Rodger  
; APPLICANT: McCallister, John  
; APPLICANT: Chiswell, David  
; APPLICANT: Darsley, Michael J.  
; APPLICANT: Fitzgerald, Kevin  
; APPLICANT: Kerten, John H.

APPLICANT: Martin, Mark T.  
APPLICANT: Titmas, Richard C.  
APPLICANT: Williams, Richard O.  
TITLE OF INVENTION: The Isolation and Production of  
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IGEN, Inc.  
STREET: 1530 East Jefferson St.  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20852  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/888,366  
FILING DATE: 03-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

OY 1 RASODIGNSL 10  
|||:|  
Db 16 RASODIGNSL 25

RESULT 10  
US-08-888-366-14  
; Sequence 14, Application US/08888366  
; Patent No. 5972656  
; GENERAL INFORMATION:  
; APPLICANT: Lopez, Oswaldo  
; APPLICANT: Wylie, Dwane E.  
; APPLICANT: Wagner, Fred W.  
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/888,366  
; FILING DATE: 03-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

Query Match 81.1%; Score 43; DB 2; Length 92;  
Best Local Similarity 90.0%; Pred. No. 0.26;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



APPLICATION NUMBER: US 08/187,407  
FILING DATE: 27-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,542  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/493,299  
FILING DATE: 14-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/324,392  
FILING DATE: 14-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648.39USC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-888-366-14

Query Match 81.1%; Score 43; DB 2; Length 107;  
Best Local Similarity 90.0%; Pred. No. 0.31;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
DB 24 RASQDIGSSL 33

RESULT 11  
US-08-888-366-20  
Sequence 20, Application US/08888366  
Patent No. 5972656  
GENERAL INFORMATION:  
APPLICANT: Lopez, Oswaldo  
APPLICANT: Wylie, Dwane E.  
APPLICANT: Wagner, Fred W.  
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESS: Merchant & Gould  
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/888,366  
FILING DATE: 03-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/187,407  
FILING DATE: 27-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,542  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/493,299  
FILING DATE: 14-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/324,392  
FILING DATE: 14-MAR-1989

ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648.39USC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-888-366-20

Query Match 81.1%; Score 43; DB 2; Length 107;  
Best Local Similarity 90.0%; Pred. No. 0.31;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
DB 24 RASQDIGSSL 33

RESULT 12  
US-08-888-366-26  
Sequence 26, Application US/08888366  
Patent No. 5972656  
GENERAL INFORMATION:  
APPLICANT: Lopez, Oswaldo  
APPLICANT: Wylie, Dwane E.  
APPLICANT: Wagner, Fred W.  
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESS: Merchant & Gould  
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/888,366  
FILING DATE: 03-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/187,407  
FILING DATE: 27-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,542  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/493,299  
FILING DATE: 14-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/324,392  
FILING DATE: 14-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648.39USC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-888-366-26

Query Match  
Best Local Similarity 90.0%; Score 43; DB 2; Length 107;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
Db 24 RASQDIGSSL 33

RESULT 13  
US-09-726-219A-267  
Sequence 267, Application US/09726219A  
GENERAL INFORMATION:  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John  
APPLICANT: Pope, Anthony  
APPLICANT: Johnson, Kevin  
APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Griffiths, Andrew  
APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kasper  
APPLICANT: Marks, James  
APPLICANT: Clackson, Timothy  
APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory  
APPLICANT: Bonert, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
FILE REFERENCE: 213839-00013  
CURRENT APPLICATION NUMBER: US/09/726,219A  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: GB 9015198.6  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6  
PRIOR FILING DATE: 1990-11-12  
PRIOR APPLICATION NUMBER: GB 9104744.9  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-08  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 267  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: light chain from clone M1F  
US-09-726-219A-267

Query Match  
Best Local Similarity 90.0%; Score 43; DB 4; Length 108;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
Db 24 RASQDIGSSL 33

RESULT 14  
US-08-713-939A-74  
Sequence 74, Application US/08713939A  
Patent No. 5846533  
GENERAL INFORMATION:  
APPLICANT: Prusiner, Stanley B.  
APPLICANT: Williamson, R. Anthony  
APPLICANT: Burton, Dennis R.  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94025

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/713,939A  
FILING DATE: 13-SEP-1996  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bozicevic, Karl  
REGISTRATION NUMBER: 28,807  
REFERENCE/DOCKET NUMBER: 06510/059001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-5277  
TELEFAX: 415-854-0875

TELEX:  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-713-939A-74

Query Match  
Best Local Similarity 90.0%; Score 43; DB 2; Length 109;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
Db 24 RASQDIGSSL 33

RESULT 15  
US-09-036-579-74  
Sequence 74, Application US/09036579  
Patent No. 6290954  
GENERAL INFORMATION:  
APPLICANT: Prusiner, Stanley B.  
APPLICANT: Williamson, R. Anthony  
APPLICANT: Burton, Dennis R.  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94025

QY 1 RASQDIGNSL 10  
Db 24 RASQDIGSSL 33

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/036,579  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/713,939  
FILING DATE: 13-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bozicevic, Karl  
REGISTRATION NUMBER: 28,807  
REFERENCE/DOCKET NUMBER: 06510/059001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-5277  
TELEFAX: 415-854-0875  
TELEX:  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-036-579-74

Query Match 81.1%; Score 43; DB 3; Length 109;  
Best Local Similarity 90.0%; Pred. No. 0.31;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQDIGNSL 10  
|||:|  
Db 24 RASQDIGSSL 33

Search completed: April 4, 2005, 16:00:51  
Job time : 6.623 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 3.06709 Seconds  
(without alignments)  
146.032 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_99\_104  
Perfect score: 34  
Sequence: 1 RFGPAY 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep: \*  
3: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep: \*  
4: /cgn2\_6/prodata/1/1aa/6C\_COMB.pep: \*  
5: /cgn2\_6/prodata/1/1aa/6CTUS\_COMB.pep: \*  
6: /cgn2\_6/prodata/1/1aa/Backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	115	3	US-08-483-749A-24
2	34	100.0	243	1	US-08-133-804-6
3	34	100.0	243	1	US-08-461-838-6
4	34	100.0	243	2	US-08-461-386-6
5	34	100.0	243	2	US-08-356-786-4
6	34	100.0	453	4	US-09-724-797-32
7	34	100.0	534	2	US-08-356-786-10
8	30	88.2	571	4	US-09-252-991A-28549
9	30	88.2	776	4	US-09-165-396-3
10	30	88.2	858	4	US-09-134-000C-5428
11	29	85.3	78	4	US-09-248-796A-25202
12	29	85.3	351	4	US-09-543-681A-6862
13	29	85.3	404	4	US-09-153-599A-8
14	29	85.3	408	4	US-09-328-352-6014
15	29	85.3	500	4	US-09-248-796A-14502
16	29	85.3	514	3	US-09-066-047-3
17	29	85.3	594	3	US-08-581-148C-14
18	29	85.3	885	3	US-09-107-532A-5104
19	28	82.4	60	4	US-09-248-796A-25174
20	28	82.4	83	4	US-09-270-767-35045
21	28	82.4	83	4	US-09-252-991A-50262
22	28	82.4	138	4	US-09-252-991A-17424
23	28	82.4	172	1	US-07-949-812-9
24	28	82.4	172	2	US-08-943-814-2
25	28	82.4	173	2	US-08-702-703-2
26	28	82.4	173	2	US-08-943-814-10
27	28	82.4	332	4	US-09-107-433-3771

28	28	82.4	396	3	US-09-134-001C-4580	Sequence 4580, Ap
29	28	82.4	409	4	US-09-583-110-3394	Sequence 3394, Ap
30	28	82.4	451	4	US-09-902-540-15200	Sequence 15200, A
31	28	82.4	689	4	US-09-902-540-14254	Sequence 14254, A
32	28	82.4	815	4	US-09-489-039A-12469	Sequence 12469, A
33	28	82.4	824	4	US-09-252-991A-18601	Sequence 18601, A
34	28	82.4	827	4	US-09-543-681A-6425	Sequence 6425, Ap
35	27	79.4	68	4	US-09-328-352-60066	Sequence 60066, Ap
36	27	79.4	138	4	US-09-328-352-8007	Sequence 8007, Ap
37	27	79.4	149	4	US-09-543-681A-8072	Sequence 8072, Ap
38	27	79.4	154	4	US-09-583-110-5042	Sequence 5042, Ap
39	27	79.4	158	4	US-09-107-433-4659	Sequence 4659, Ap
40	27	79.4	178	4	US-09-328-352-7054	Sequence 7054, Ap
41	27	79.4	211	4	US-09-489-039A-9497	Sequence 9497, Ap
42	27	79.4	215	4	US-09-902-540-10983	Sequence 10983, Ap
43	27	79.4	262	4	US-09-949-016-10824	Sequence 10824, A
44	27	79.4	262	4	US-09-949-016-10825	Sequence 10825, A
45	27	79.4	262	4	US-09-949-016-10826	Sequence 10826, A

ALIGNMENTS

RESULT 1  
US-08-483-749A-24  
Sequence 24, Application US/08483749A  
Patent No. 6054561  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OR INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESSES:  
ADDRESS: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
CITY: EMERYVILLE  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,749A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVERIDE, PAUL B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0508.008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-749A-24  
Query Match 100.0%; Score 34; DB 3; Length 115;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RFGPAY 6  
DB 99 RFGPAY 104  
RESULT 2

US-08-133-804-6  
; Sequence 6, Application US/08133804  
; Patent No. 5534254  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Proteins For  
; TITLE OF INVENTION: Imaging  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/133,804  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kelley, Robin D.  
; REGISTRATION NUMBER: 34,637  
; REFERENCE/DOCKET NUMBER: 2054/22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-248-7477  
; TELEFAX: 617-248-7100  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 243 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-133-804-6  
Query Match 100.0%; Score 34; DB 1; Length 243;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RFGFAY 6  
Db 99 RFGFAY 104  
RESULT 3  
US-08-461-838-6  
; Sequence 6, Application US/08461838  
; Patent No. 5753204  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Proteins For  
; TITLE OF INVENTION: Imaging  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,838  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kelley, Robin D.  
; REGISTRATION NUMBER: 34,637  
; REFERENCE/DOCKET NUMBER: 2054/22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-248-7477  
; TELEFAX: 617-248-7100  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 243 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-461-838-6  
Query Match 100.0%; Score 34; DB 1; Length 243;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RFGFAY 6  
Db 99 RFGFAY 104  
RESULT 4  
US-08-461-386-6  
; Sequence 6, Application US/08461386  
; Patent No. 5837846  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Proteins For  
; TITLE OF INVENTION: Imaging  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,386  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kelley, Robin D.  
; REGISTRATION NUMBER: 34,637  
; REFERENCE/DOCKET NUMBER: 2054/22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-248-7477  
; TELEFAX: 617-248-7100  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 243 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-461-386-6

Query Match 100.0%; Score 34; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRGPAY 6  
Db 99 RRGPAY 104

## RESULT 5

US-08-356-786-4  
Sequence 4, Application US/08356786  
Patent No. 5877305

## GENERAL INFORMATION:

APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
TITLE OF INVENTION: Marker  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,786  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/831,967  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
REGISTRATION NUMBER: 27,829  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-786-4

Query Match 100.0%; Score 34; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRGPAY 6  
Db 99 RRGPAY 104

## RESULT 6

US-09-724-797-32  
Sequence 32, Application US/09724797  
Patent No. 6733998

GENERAL INFORMATION:  
APPLICANT: Jon S. THORSON  
TITLE OF INVENTION: MICROMONOPORA ECHINOSPORA GENES  
TITLE OF INVENTION: ENCODING FOR BIOSYNTHESIS OF  
TITLE OF INVENTION: CALICHEMICIN AND SELF-RESISTANCE THERETO

FILE REFERENCE: 2653-40  
CURRENT APPLICATION NUMBER: US/09/724,797  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 60/111,325  
PRIOR FILING DATE: 1998-12-07  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32  
LENGTH: 453  
TYPE: PRT  
ORGANISM: Bacteria  
US-09-724-797-32

## Query Match

100.0%; Score 34; DB 4; Length 453;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRGPAY 6  
Db 443 RRGPAY 448

## RESULT 7

US-08-356-786-10  
Sequence 10, Application US/08356786  
Patent No. 5877305

## GENERAL INFORMATION:

APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
TITLE OF INVENTION: Marker  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,786  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/831,967  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
REGISTRATION NUMBER: 27,829  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 534 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-786-10

Query Match 100.0%; Score 34; DB 2; Length 534;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRGPAY 6

Db 388 RRGFAY 393

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RESULT 8
US-09-252-991A-28549
; Sequence 28549, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28549
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28549
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Query Match 88.2%; Score 30; DB 4; Length 571;  
Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6  
Db 348 RRGFAY 353

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RESULT 9
US-09-165-396-3
; Sequence 3, Application US/09165396
; Patent No. 6441134
; GENERAL INFORMATION:
; APPLICANT: BECKER, JEFFREY W.
; APPLICANT: LUBKOWITZ, MARK A.
; TITLE OF INVENTION: ISOLATED CANDIDA ALBICANS OLIGOPEPTIDE TRANSPORTER GENE
; FILE REFERENCE: 372.6520P
; CURRENT APPLICATION NUMBER: US/09/165,396
; EARLIER FILING DATE: 1998-10-02
; EARLIER APPLICATION NUMBER: PCT/US98/02332
; EARLIER FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: 60/037,859
; EARLIER FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 776
; TYPE: PRT
; ORGANISM: S. pombe
US-09-165-396-3
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Query Match 88.2%; Score 30; DB 4; Length 776;  
Best Local Similarity 83.3%; Pred. No. 3.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGFAY 6  
Db 195 RRGFAY 200

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RESULT 10
US-09-134-000C-5428
; Sequence 5428, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
```

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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5428
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5428
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Query Match 88.2%; Score 30; DB 4; Length 858;  
Best Local Similarity 83.3%; Pred. No. 3.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6  
Db 139 QRGFAY 144

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RESULT 11
US-09-248-796A-25202
; Sequence 25202, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 25202
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-25202
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Query Match 85.3%; Score 29; DB 4; Length 78;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRGFAY 6  
Db 74 RRGFAY 78

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RESULT 12
US-09-543-681A-6862
; Sequence 6862, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6862
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Proteus mirabilis
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US-09-543-681A-6862

Query Match 85.3%; Score 29; DB 4; Length 351;  
Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGPAY 6  
DB 243 RRGFLY 248

RESULT 13

US-09-153-599A-8  
Sequence 8, Application US/09153599A  
Patent No. 6420177

GENERAL INFORMATION:  
APPLICANT: Weber, J. Mark  
APPLICANT: Lau, B. Minh  
TITLE OF INVENTION: Method for Strain Improvement of  
TITLE OF INVENTION: Erythromycin Producing Bacterium  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Rokey, Milnamow & Katz, Ltd.  
STREET: 180 N. Steetson Avenue, 2 Prudential Plaza  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/153,599A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mueller, Lisa V.  
REGISTRATION NUMBER: 38,978  
REFERENCE/DOCKET NUMBER: FER2159P0041US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5400  
TELEFAX: 312-616-5460  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 404 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-153-599A-8

Query Match 85.3%; Score 29; DB 4; Length 404;  
Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGPAY 6  
DB 49 RRGFLY 54

RESULT 14

US-09-328-352-6014  
Sequence 6014, Application US/09328352  
Patent No. 6562958

GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 6014  
LENGTH: 408  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-6014

Query Match 85.3%; Score 29; DB 4; Length 408;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRGPAY 6  
DB 317 RRGFLY 321

RESULT 15

US-09-248-796A-14502  
Sequence 14502, Application US/09248796A  
Patent No. 6747137

GENERAL INFORMATION:  
APPLICANT: Keith Weinstein et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
CURRENT FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 14502  
LENGTH: 500  
TYPE: PRT  
ORGANISM: Candida albicans  
US-09-248-796A-14502

Query Match 85.3%; Score 29; DB 4; Length 500;  
Best Local Similarity 83.3%; Pred. No. 3.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGPAY 6  
DB 275 RRGFLY 280

Search completed: April 4, 2005, 16:00:53  
Job time : 4.06709 secs

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US-08-133-804-6
; Sequence 6, Application US/08133804
; Patent No. 5534254
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-133-804-6
Query Match 100.0%; Score 97; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 4,4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WINTYGOSTYADDFKE 17
DB 50 WINTYGOSTYADDFKE 66
RESULT 3
US-08-461-838-6
; Sequence 6, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,386
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-461-838-6
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,838
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-838-6
```

```
Query Match 100.0%; Score 97; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 4,4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 WINTYGOSTYADDFKE 17
DB 50 WINTYGOSTYADDFKE 66
```

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RESULT 4
US-08-461-386-6
; Sequence 6, Application US/08461386
; Patent No. 5837846
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,386
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-461-386-6
```

Query Match 100.0%; Score 97; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGSTYADDFKE 17  
|||||  
DB 50 WINTYGSTYADDFKE 66

## RESULT 5

US-08-356-786-4  
; Sequence 4, Application US/08356786  
; Patent No. 5877305  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
; TITLE OF INVENTION: Marker  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSES: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/356,786  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/831,967  
; FILING DATE: 06-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pitcher, Edmund R.  
; REGISTRATION NUMBER: 27,829  
; REFERENCE/DOCKET NUMBER: CRP-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 243 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-356-786-4

Query Match 100.0%; Score 97; DB 2; Length 243;

Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGSTYADDFKE 17  
|||||  
DB 50 WINTYGSTYADDFKE 66

## RESULT 6

US-08-356-786-10  
; Sequence 10, Application US/08356786  
; Patent No. 5877305  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
; TITLE OF INVENTION: Marker  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSES: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/356,786  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/831,967  
; FILING DATE: 06-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pitcher, Edmund R.  
; REGISTRATION NUMBER: 27,829  
; REFERENCE/DOCKET NUMBER: CRP-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 534 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-356-786-10

Query Match 100.0%; Score 97; DB 2; Length 534;

Best Local Similarity 100.0%; Pred. No. 9.8e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGSTYADDFKE 17  
|||||  
DB 339 WINTYGSTYADDFKE 355

## RESULT 7

US-08-875-811-53  
; Sequence 53, Application US/08875811  
; Patent No. 6045793  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Diane L.  
; APPLICANT: Boque, Lluís  
; APPLICANT: Wlodawer, Alexander  
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSES: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/875,811  
; FILING DATE: 19-FEB-1998  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Fairis, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-53

Query Match  
Best Local Similarity 91.8%; Score 89; DB 3; Length 365;  
Best Local Similarity 93.8%; Pred. No. 1.1e-05;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYTGOSTYADDFK 16  
|||||:|||||  
Db 168 WINTYTGESTYADDFK 183

RESULT 8  
US-08-875-811-55  
Sequence 55, Application US/08875811  
GENERAL INFORMATION:  
PATENT No. 6045793  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Lluís  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Fairis, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 366 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-55

Query Match  
Best Local Similarity 91.8%; Score 89; DB 3; Length 366;  
Best Local Similarity 93.8%; Pred. No. 1.1e-05;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYTGOSTYADDFK 16  
|||||:|||||  
Db 51 WINTYTGESTYADDFK 66

RESULT 9  
US-08-279-772A-6  
Sequence 6, Application US/08279772A  
Patent No. 6080560  
GENERAL INFORMATION:  
APPLICANT: Russell, David R.  
APPLICANT: Fuller, James T.  
TITLE OF INVENTION: Method for Producing Antibodies in Plant  
TITLE OF INVENTION: Cells  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Quarles and Brady  
STREET: PO Box 2113  
CITY: Madison  
STATE: WI  
COUNTRY: United States of America  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/279,772A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386  
REFERENCE/DOCKET NUMBER: 11-229-9097-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-279-772A-6

Query Match  
Best Local Similarity 89.7%; Score 87; DB 3; Length 252;  
Best Local Similarity 93.8%; Pred. No. 1.5e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGOSTYADDFK 16  
|||||:|||||  
Db 180 WINTYTGOSTYADDFK 195

RESULT 10  
US-08-902-486-9  
Sequence 9, Application US/08902486  
Patent No. 6140075  
GENERAL INFORMATION:  
APPLICANT: Russell, David R.  
APPLICANT: Fuller, James T.  
TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND  
TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS

NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,486  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 670513.90261  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-902-486-9

Query Match 89.7%; Score 87; DB 3; Length 252;  
Best Local Similarity 93.8%; Pred. No. 1.5e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYGOSTYADDFK 16  
Db 180 WINTYGOSTYADDFK 195

RESULT 11  
US-09-485-737B-102  
Sequence 102, Application US/09485737B  
Patent No. 6350860  
GENERAL INFORMATION:  
APPLICANT: Buyse, Marie-Ange  
TITLE OF INVENTION: INTERPERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,  
FILE REFERENCE: INNS:015  
CURRENT APPLICATION NUMBER: US/09/485,737B  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
PRIOR FILING DATE: 1998-08-14  
PRIOR APPLICATION NUMBER: EPO 98870139.7  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: EPO 97870122.5  
PRIOR FILING DATE: 1997-08-18  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 102  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: SYNTHETIC  
US-09-485-737B-102

Query Match 87.6%; Score 85; DB 3; Length 230;  
Best Local Similarity 87.5%; Pred. No. 2.7e-05;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYGOSTYADDFK 16  
Db 50 WINTYGESTYVDDFK 65

RESULT 12  
US-10-071-485-102  
Sequence 102, Application US/10071485  
Patent No. 6830752  
GENERAL INFORMATION:  
APPLICANT: Buyse, Marie-Ange  
TITLE OF INVENTION: INTERPERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC  
SHOCK,  
FILE REFERENCE: INNS:015  
CURRENT APPLICATION NUMBER: US/10/071,485  
PRIOR FILING DATE: 2002-02-07  
PRIOR APPLICATION NUMBER: 09/485,737  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
PRIOR FILING DATE: 1998-08-14  
PRIOR APPLICATION NUMBER: EPO 98870139.7  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: EPO 97870122.5  
PRIOR FILING DATE: 1997-08-18  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 102  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: SYNTHETIC  
US-10-071-485-102

Query Match 87.6%; Score 85; DB 4; Length 230;  
Best Local Similarity 87.5%; Pred. No. 2.7e-05;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYGOSTYADDFK 16  
Db 50 WINTYGESTYVDDFK 65

RESULT 13  
US-09-485-737B-93  
Sequence 93, Application US/09485737B  
Patent No. 6350860  
GENERAL INFORMATION:  
APPLICANT: Buyse, Marie-Ange  
TITLE OF INVENTION: INTERPERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,  
FILE REFERENCE: INNS:015  
CURRENT APPLICATION NUMBER: US/09/485,737B  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
PRIOR FILING DATE: 1998-08-14  
PRIOR APPLICATION NUMBER: EPO 98870139.7  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: EPO 97870122.5  
PRIOR FILING DATE: 1997-08-18  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 93  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: SYNTHETIC  
US-09-485-737B-93

Query Match 87.6%; Score 85; DB 3; Length 235;  
Best Local Similarity 87.5%; Pred. No. 2.8e-05;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGOSTYADDFK 16  
|||||:|||||  
Db 50 WINTYTGESTYVDDFK 65

RESULT 14  
US-10-071-485-93  
; Sequence 93, Application US/10071485  
; Patent No. 6830752

GENERAL INFORMATION:  
; APPLICANT: Buyse, Marie-Ange  
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC  
; TITLE OF INVENTION: SHOCK,  
; FILE REFERENCE: INNS:015  
; CURRENT APPLICATION NUMBER: US/10/071,485  
; CURRENT FILING DATE: 2002-02-07  
; PRIOR APPLICATION NUMBER: 09/485,737  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
; PRIOR FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: EPO 98870139.7  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: EPO 97870122.5  
; PRIOR FILING DATE: 1997-08-18  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 93  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC  
US-10-071-485-93

Query Match 87.6%; Score 85; DB 4; Length 235;  
Best Local Similarity 87.5%; Pred. No. 2.8e-05;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGOSTYADDFK 16  
|||||:|||||  
Db 50 WINTYTGESTYVDDFK 65

RESULT 15  
US-09-485-737B-91  
; Sequence 91, Application US/09485737B  
; Patent No. 6350860

GENERAL INFORMATION:  
; APPLICANT: Buyse, Marie-Ange  
; APPLICANT: Sablon, Erwin  
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,  
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
; FILE REFERENCE: INNS:015  
; CURRENT APPLICATION NUMBER: US/09/485,737B  
; CURRENT FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
; PRIOR FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: EPO 98870139.7  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: EPO 97870122.5  
; PRIOR FILING DATE: 1997-08-18  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 91  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: SYNTHETIC  
US-09-485-737B-91

Query Match 87.6%; Score 85; DB 3; Length 240;  
Best Local Similarity 87.5%; Pred. No. 2.8e-05;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGOSTYADDFK 16  
|||||:|||||  
Db 50 WINTYTGESTYVDDFK 65

Search completed: April 4, 2005, 16:00:50  
Job time : 8.6901 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 2.55591 Seconds  
(without alignments) 146.032 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_31\_35

Perfect score: 30

Sequence: 1 NYGMN 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	5	3	US-08-783-853A-8
2	30	100.0	5	3	US-09-344-050-8
3	30	100.0	74	3	US-09-134-001C-3503
4	30	100.0	92	3	US-08-783-853A-84
5	30	100.0	92	3	US-09-344-050-84
6	30	100.0	112	3	US-08-783-853A-20
7	30	100.0	112	3	US-09-344-050-20
8	30	100.0	115	3	US-08-483-749A-24
9	30	100.0	117	1	US-08-249-013-6
10	30	100.0	117	2	US-08-866-863-6
11	30	100.0	117	3	US-09-175-229-6
12	30	100.0	117	5	PCT-US95-06764-6
13	30	100.0	118	1	US-08-425-336-124
14	30	100.0	118	1	US-08-425-336-126
15	30	100.0	118	1	US-08-488-113B-124
16	30	100.0	118	1	US-08-488-113B-126
17	30	100.0	118	1	US-08-477-484B-124
18	30	100.0	118	1	US-08-477-484B-126
19	30	100.0	118	1	US-08-107-669D-28
20	30	100.0	118	1	US-08-107-669D-29
21	30	100.0	118	1	US-08-107-669D-65
22	30	100.0	118	1	US-08-107-669D-67
23	30	100.0	118	1	US-08-472-788A-28
24	30	100.0	118	1	US-08-472-788A-29
25	30	100.0	118	1	US-08-472-788A-88
26	30	100.0	118	1	US-08-472-788A-89
27	30	100.0	118	2	US-08-477-531B-28

28	30	100.0	118	2	US-08-477-531B-29	Sequence 29, Appl
29	30	100.0	118	2	US-08-477-531B-66	Sequence 66, Appl
30	30	100.0	118	2	US-08-477-531B-67	Sequence 67, Appl
31	30	100.0	118	2	US-08-646-360-124	Sequence 124, App
32	30	100.0	118	2	US-08-646-360-126	Sequence 126, App
33	30	100.0	118	2	US-08-082-842A-28	Sequence 28, Appl
34	30	100.0	118	2	US-08-082-842A-29	Sequence 29, Appl
35	30	100.0	118	2	US-08-082-842A-88	Sequence 88, Appl
36	30	100.0	118	2	US-08-082-842A-89	Sequence 89, Appl
37	30	100.0	118	3	US-08-839-765-124	Sequence 124, App
38	30	100.0	118	3	US-08-839-765-126	Sequence 126, App
39	30	100.0	118	3	US-09-136-389-124	Sequence 124, App
40	30	100.0	118	3	US-09-136-389-126	Sequence 126, App
41	30	100.0	118	3	US-09-610-838-124	Sequence 124, App
42	30	100.0	118	3	US-09-610-838-126	Sequence 126, App
43	30	100.0	118	4	US-09-440-781-96	Sequence 96, Appl
44	30	100.0	118	4	US-09-711-485-124	Sequence 124, App
45	30	100.0	118	4	US-09-711-485-126	Sequence 126, App

#### ALIGNMENTS

RESULT 1  
US-08-783-853A-8  
Sequence 8, Application US/08783853A  
Patent No. 6005091  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Gloria  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/783, 853A  
FILING DATE: 16-JAN-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/029,119  
FILING DATE: 24-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-783-853A-8

Query Match 100.0%; Score 30; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 1 NYGMN 5

RESULT 2  
US-09-344-050-8  
Sequence 8, Application US/09344050  
Patent No. 6391299  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Gloria  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/344,050  
FILING DATE: 24-JUN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/783,853  
FILING DATE: 16-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-09-344-050-8  
Query Match 100.0%; Score 30; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
Db 1 NYGMN 5

RESULT 3  
US-09-134-001C-3503  
Sequence 3503, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3503  
LENGTH: 74  
TYPE: prf  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3503

Query Match 100.0%; Score 30; DB 3; Length 74;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 4 NYGMN 8

RESULT 4  
US-08-783-853A-84  
Sequence 84, Application US/08783853A  
Patent No. 6005091  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Gloria  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/783,853A  
FILING DATE: 16-JAN-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/029,119  
FILING DATE: 24-OCT-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
US-08-783-853A-84

Query Match 100.0%; Score 30; DB 3; Length 92;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5  
Db 8 NYGMN 12

RESULT 5  
US-09-344-050-84  
Sequence 84, Application US/09344050  
Patent No. 6391299  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Gloria  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/344,050  
FILING DATE: 24-JUN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/783,853  
FILING DATE: 16-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:

INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
US-09-344-050-84

Query Match 100.0%; Score 30; DB 3; Length 92;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5  
Db 8 NYGMN 12

RESULT 6  
US-08-783-853A-20  
Sequence 20, Application US/08783853A  
Patent No. 6003091  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Gloria  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/783,853A  
FILING DATE: 16-JAN-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/029,119  
FILING DATE: 24-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-783-853A-20

Query Match 100.0%; Score 30; DB 3; Length 112;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 28 NYGMN 32

RESULT 7  
US-09-344-050-20  
Sequence 20, Application US/09344050  
Patent No. 6391299  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Giora  
APPLICANT: Nichols, Andrew  
APPLICANT: Padiam, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/344,050  
FILING DATE: 24-JUN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/783,853  
FILING DATE: 16-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-09-344-050-20

Query Match 100.0%; Score 30; DB 3; Length 112;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 28 NYGMN 32

RESULT 8  
US-08-483-749A-24  
Sequence 24, Application US/08483749A  
Patent No. 6054561  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
CITY: EMERYVILLE  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,749A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVEREIDE, PAUL B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0508.008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-749A-24

Query Match 100.0%; Score 30; DB 3; Length 115;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 31 NYGMN 35

RESULT 9  
US-08-249-013-6  
Sequence 6, Application US/08249013  
Patent No. 5643754  
GENERAL INFORMATION:  
APPLICANT: Haake, David A.  
TITLE OF INVENTION: CLONED leptospira OUTER MEMBRANE PROTEIN  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/249,013  
FILING DATE: 25-MAY-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Tumarkin Ph.D., Lisa A.,  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: PD-3602  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: lufa  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..117  
US-08-249-013-6

Query Match 100.0%; Score 30; DB 1; Length 117;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 22 NYGMN 26

RESULT 10  
US-08-866-863-6  
Sequence 6, Application US/0886863  
Patent No. 5824321  
GENERAL INFORMATION:  
APPLICANT: Haake, David A.  
TITLE OF INVENTION: CLONED Leptospira OUTER MEMBRANE PROTEIN  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/886,863  
FILING DATE: 01-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/249,013  
FILING DATE: 25-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Tumarkin Ph.D., Lisa A.,  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: PD-3602  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: lufa  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..117  
US-08-866-863-6

Query Match 100.0%; Score 30; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 22 NYGMN 26

RESULT 11  
US-09-175-229-6  
Sequence 6, Application US/09175229  
Patent No. 6309641  
GENERAL INFORMATION:  
APPLICANT: Haake, David A.  
TITLE OF INVENTION: CLONED Leptospira OUTER MEMBRANE PROTEIN  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/175,229  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/249,013  
FILING DATE: 25-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Tumarkin Ph.D., Lisa A.,  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: PD-3602  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: lufa  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..117  
US-09-175-229-6

Query Match 100.0%; Score 30; DB 3; Length 117;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 22 NYGMN 26

## RESULT 12

PCT-US95-06764-6  
Sequence 6, Application PC/TUS9506764

GENERAL INFORMATION:  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: CLONED Leptospira OUTER MEMBRANE PROTEIN  
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla  
STATE: California

COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06764  
FILING DATE: 25-MAY-1995

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:

NAME: Hallie, Ph.D., Lisa A.,  
REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: FD3602  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 678-5070  
TELEFAX: (619) 678-5099

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
IMMEDIATE SOURCE:

CLONE: lnta  
FEATURE:

NAME/KEY: Protein  
LOCATION: 1..117

PCT-US95-06764-6

Query Match 100.0%; Score 30; DB 5; Length 117;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 22 NYGMN 26

## RESULT 13

US-08-425-336-124  
Sequence 124, Application US/08425336  
Patent No. 5621083

GENERAL INFORMATION:

APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago  
STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,336  
FILING DATE: 18-APR-1995

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/064,691  
FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.

REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 31394

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448

TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 124:

SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids

TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-425-336-124

Query Match 100.0%; Score 30; DB 1; Length 118;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 31 NYGMN 35

## RESULT 14

US-08-425-336-126  
Sequence 126, Application US/08425336  
Patent No. 5621083

GENERAL INFORMATION:

APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago  
STATE: Illinois

COUNTRY: USA  
ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,336  
FILING DATE: 18-APR-1995

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 31394  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-425-336-126

Query Match 100.0%; Score 30; DB 1; Length 118;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 31 NYGMN 35

RESULT 15  
US-08-488-113B-124  
Sequence 124, Application US/08488113B  
Patent No. 5744580  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSER: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-124

Query Match 100.0%; Score 30; DB 1; Length 118;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 31 NYGMN 35

Search completed: April 4, 2005, 16:00:50  
Job time : 3.55591 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 124.217 seconds  
(without alignments)  
146.032 Million cell updates/sec

Title: US-09-887-853-6

Perfect score: 1258

Sequence: 1 EIQLVOSGPELKKPGETVTKI.....YAIFFYFGGNNLEIKRAD 243

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: \*  
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2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1258	100.0	243	1	US-08-133-804-6	Sequence 6, Appl1
2	1258	100.0	243	1	US-08-461-838-6	Sequence 6, Appl1
3	1258	100.0	243	1	US-08-461-386-6	Sequence 6, Appl1
4	1258	100.0	243	2	US-08-356-786-4	Sequence 4, Appl1
5	1214	96.5	534	2	US-08-356-786-10	Sequence 10, Appl1
6	914	72.7	250	1	US-08-133-804-2	Sequence 2, Appl1
7	914	72.7	250	1	US-08-461-184-8	Sequence 8, Appl1
8	914	72.7	250	1	US-08-463-675-8	Sequence 8, Appl1
9	914	72.7	250	1	US-08-464-589-8	Sequence 8, Appl1
10	914	72.7	250	1	US-08-461-838-2	Sequence 2, Appl1
11	914	72.7	250	2	US-08-461-386-2	Sequence 2, Appl1
12	891	70.8	622	2	US-08-356-786-16	Sequence 16, Appl1
13	827	65.7	240	1	US-08-489-113B-148	Sequence 148, App
14	827	65.7	240	1	US-08-477-484B-148	Sequence 148, App
15	827	65.7	240	2	US-08-646-360-148	Sequence 148, App
16	827	65.7	240	3	US-08-839-765-148	Sequence 148, App
17	827	65.7	240	3	US-09-136-389-148	Sequence 148, App
18	827	65.7	240	3	US-09-610-838-148	Sequence 148, App
19	827	65.7	240	4	US-09-711-485-148	Sequence 148, App
20	823.5	65.5	530	4	US-08-840-713-2	Sequence 2, Appl1
21	823.5	65.5	615	4	US-08-840-713-35	Sequence 35, Appl1
22	823.5	65.5	617	4	US-08-840-713-37	Sequence 37, Appl1
23	823.5	65.5	637	2	US-08-235-838-14	Sequence 14, Appl1
24	823.5	65.5	637	2	US-08-465-473B-14	Sequence 14, Appl1
25	823.5	65.5	711	2	US-08-235-838-7	Sequence 7, Appl1
26	823.5	65.5	711	2	US-08-465-473B-7	Sequence 7, Appl1
27	818.5	65.1	241	1	US-08-235-838-5	Sequence 5, Appl1

28	818.5	65.1	241	2	US-08-465-473B-5	Sequence 5, Appl1
29	816	64.9	259	4	US-09-419-788-115	Sequence 115, App
30	804	63.9	267	3	US-09-485-737B-2	Sequence 2, Appl1
31	804	63.9	267	4	US-10-071-485-2	Sequence 85, Appl1
32	804	63.9	541	3	US-09-485-737B-85	Sequence 85, Appl1
33	804	63.9	541	4	US-10-071-485-85	Sequence 90, Appl1
34	804	63.9	711	4	US-09-485-737B-90	Sequence 90, Appl1
35	804	63.9	711	4	US-10-071-485-90	Sequence 40, Appl1
36	803	63.8	284	3	US-09-184-658-40	Sequence 40, Appl1
37	803	63.8	284	4	US-09-504-262D-40	Sequence 53, Appl1
38	799.5	63.6	365	3	US-08-875-811-53	Sequence 55, Appl1
39	799.5	63.6	366	3	US-08-875-811-55	Sequence 91, Appl1
40	791.5	62.9	240	3	US-09-485-737B-91	Sequence 91, Appl1
41	791.5	62.9	240	4	US-10-071-485-91	Sequence 91, Appl1
42	782.5	62.2	287	4	US-09-318-786-37	Sequence 37, Appl1
43	779	61.9	235	3	US-09-485-737B-93	Sequence 93, Appl1
44	779	61.9	235	4	US-10-071-485-93	Sequence 93, Appl1
45	766.5	60.9	230	3	US-09-485-737B-102	Sequence 102, App

#### ALIGNMENTS

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RESULT 1
US-08-133-804-6
; Sequence 6, Application US/08133804
; Patent No. 5534254
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Teeter, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-133-804-6

Query Match 100.0%; Score 1258; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.9e-105;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EIQLVOSGPELKKPGETVTKISKASGYTFANYGNMNMKQAPGKGLKMMGMINTYTGOSTY 60
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DB 61 ADDFKERFAFSLKPGTATTAHLQINNLRNEDSATYFCARRFGPAYWCGGTLVSVASISS 120
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DB 121 SSSSSSSSSSDIQMTQSPSSLASLGERVSLTCRASODIGNSLTWLQOEPPDGTIKRL 180
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DB 181 IYATSSLDGVPKRRSGSGSDYSLTISLSEDFVYVYCLQYALFPTFGGNTLEIK 240
QY 241 RAD 243
DB 241 RAD 243
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## RESULT 2

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US-08-461-838-6
; Sequence 6, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,838
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-838-6
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Query Match 100.0%; Score 1258; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.9e-105;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 EIQLVOSGPELKKPGTATTAHLQINNLRNEDSATYFCARRFGPAYWCGGTLVSVASISS 60
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DB 61 ADDFKERFAFSLKPGTATTAHLQINNLRNEDSATYFCARRFGPAYWCGGTLVSVASISS 120
QY 181 IYATSSLDGVPKRRSGSGSDYSLTISLSEDFVYVYCLQYALFPTFGGNTLEIK 240
DB 181 IYATSSLDGVPKRRSGSGSDYSLTISLSEDFVYVYCLQYALFPTFGGNTLEIK 240
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DB 121 SSSSSSSSSSDIQMTQSPSSLASLGERVSLTCRASODIGNSLTWLQOEPPDGTIKRL 180
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QY 241 RAD 243
DB 241 RAD 243
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## RESULT 3

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US-08-461-386-6
; Sequence 6, Application US/08461386
; Patent No. 5837846
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,386
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-386-6
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Query Match 100.0%; Score 1258; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.9e-105;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 EIQLVOSGPELKKPGTATTAHLQINNLRNEDSATYFCARRFGPAYWCGGTLVSVASISS 60
QY 61 ADDFKERFAFSLKPGTATTAHLQINNLRNEDSATYFCARRFGPAYWCGGTLVSVASISS 120
DB 61 ADDFKERFAFSLKPGTATTAHLQINNLRNEDSATYFCARRFGPAYWCGGTLVSVASISS 120
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DB 121 SSSSSSSSSSDIQMTQSPSSLASLGERVSLTCRASODIGNSLTWLQOEPPDGTIKRL 180
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DB 181 IYATSSLDGVPKRRSGSGSDYSLTISLSEDFVYVYCLQYALFPTFGGNTLEIK 240
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Db 181 IYATSSLDGCVPRFSGSRSSGSDYSLTISLSESDPVVYVCLOYAFPTTGGGNTLEIK 240  
QY 241 RAD 243  
Db 241 RAD 243

RESULT 4  
US-08-356-786-4  
/ Sequence 4, Application US/08356786  
/ Patent No. 5877305  
/ GENERAL INFORMATION:  
/ APPLICANT: Huston, James S.  
/ APPLICANT: Oppermann, Hermann  
/ APPLICANT: Houston, L. L.  
/ APPLICANT: Ring, David B.  
/ TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
/ NUMBER OF SEQUENCES: 16  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
/ STREET: Exchange Place, 53 State Street  
/ CITY: Boston  
/ STATE: Massachusetts  
/ COUNTRY: USA  
/ ZIP: 02109  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patentin Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/356,786  
/ FILING DATE:  
/ CLASSIFICATION: 424  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 07/831,967  
/ FILING DATE: 06-FEB-1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Pitcher, Edmund R.  
/ REGISTRATION NUMBER: 27,829  
/ REFERENCE/DOCKET NUMBER: CRP-053  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (617) 248-7000  
/ TELEFAX: (617) 248-7100  
/ INFORMATION FOR SEQ ID NO: 4:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 243 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ US-08-356-786-4

Query Match 100.0%; Score 1258; DB 2; Length 243;

Best Local Similarity 100.0%; Pred. No. 3.9e-105; Mismatches 0; Indels 0; Gaps 0;

Db 1 EIQLVQSGPELKKPEETVYKISCKASGYTFPANYGMMMKQAPGKGLKMMGINTYTGOSTY 60  
QY 1 EIQLVQSGPELKKPEETVYKISCKASGYTFPANYGMMMKQAPGKGLKMMGINTYTGOSTY 60  
Db 1 EIQLVQSGPELKKPEETVYKISCKASGYTFPANYGMMMKQAPGKGLKMMGINTYTGOSTY 60  
QY 61 ADDPKERAFSLSETATTAHLQINNLRNEDSATYFCARRFGAYVGGGTLVSVASISSS 120  
Db 61 ADDPKERAFSLSETATTAHLQINNLRNEDSATYFCARRFGAYVGGGTLVSVASISSS 120  
QY 61 ADDPKERAFSLSETATTAHLQINNLRNEDSATYFCARRFGAYVGGGTLVSVASISSS 120  
Db 61 ADDPKERAFSLSETATTAHLQINNLRNEDSATYFCARRFGAYVGGGTLVSVASISSS 120  
QY 121 SSSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWQOEPPDGTIKRL 180  
Db 121 SSSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWQOEPPDGTIKRL 180  
QY 121 SSSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWQOEPPDGTIKRL 180  
Db 121 SSSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWQOEPPDGTIKRL 180  
QY 181 IYATSSLDGCVPRFSGSRSSGSDYSLTISLSESDPVVYVCLOYAFPTTGGGNTLEIK 240  
Db 181 IYATSSLDGCVPRFSGSRSSGSDYSLTISLSESDPVVYVCLOYAFPTTGGGNTLEIK 240

QY 241 RAD 243  
Db 241 RAD 243

RESULT 5  
US-08-356-786-10  
/ Sequence 10, Application US/08356786  
/ Patent No. 5877305  
/ GENERAL INFORMATION:  
/ APPLICANT: Huston, James S.  
/ APPLICANT: Oppermann, Hermann  
/ APPLICANT: Houston, L. L.  
/ APPLICANT: Ring, David B.  
/ TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
/ NUMBER OF SEQUENCES: 16  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
/ STREET: Exchange Place, 53 State Street  
/ CITY: Boston  
/ STATE: Massachusetts  
/ COUNTRY: USA  
/ ZIP: 02109  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patentin Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/356,786  
/ FILING DATE:  
/ CLASSIFICATION: 424  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 07/831,967  
/ FILING DATE: 06-FEB-1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Pitcher, Edmund R.  
/ REGISTRATION NUMBER: 27,829  
/ REFERENCE/DOCKET NUMBER: CRP-053  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (617) 248-7000  
/ TELEFAX: (617) 248-7100  
/ INFORMATION FOR SEQ ID NO: 10:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 534 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ US-08-356-786-10

Query Match 96.5%; Score 1214; DB 2; Length 534;

Best Local Similarity 95.9%; Pred. No. 1e-100; Mismatches 8; Indels 2; Gaps 1;

QY 1 EIQLVQSGPELKKPEETVYKISCKASGYTFPANYGMMMKQAPGKGLKMMGINTYTGOSTY 60  
Db 290 EIQLVQSGPELKKPEETVYKISCKASGYTFPANYGMMMKQAPGKGLKMMGINTYTGOSTY 349  
QY 61 ADDPKERAFSLSETATTAHLQINNLRNEDSATYFCARRFGAYVGGGTLVSVASISSS 120  
Db 350 ADDPKERAFSLSETATTAHLQINNLRNEDSATYFCARRFGAYVGGGTLVSVASISSS 409  
QY 121 --SGSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWQOEPPDGTIKRL 178  
Db 410 GCGSGCGGSGGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWQOEPPDGTIKRL 469  
QY 179 RLIVATSSLDGCVPRFSGSRSSGSDYSLTISLSESDPVVYVCLOYAFPTTGGGNTLEIK 238  
Db 470 RLIVATSSLDGCVPRFSGSRSSGSDYSLTISLSESDPVVYVCLOYAFPTTGGGNTLEIK 529  
QY 239 IKRAD 243

Db 530 IKRAD 534

## RESULT 6

US-08-133-804-2

Sequence 2, Application US/08133804

Patent No. 5534254

GENERAL INFORMATION:

APPLICANT: Husecon, James S.

APPLICANT: Oppermann, Hermann

APPLICANT: Houston, L. L.

APPLICANT: Ring, David B.

TITLE OF INVENTION: Biosynthetic Binding Proteins For

TITLE OF INVENTION: Imaging

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department

STREET: Exchange Place, 53 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/133,804

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Kelley, Robin D.

REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: 2054/22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7477

TELEFAX: 617-248-7100

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 250 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-133-804-2

Query Match 72.7%; Score 914; DB 1; Length 250;  
Best Local Similarity 71.7%; Pred. No. 3.1e-74;  
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

QY 1 EIQLVSGPELKKRGRTYKISCKASGYTFANYGMNMKQAPGKGLKMMGWINTYTGQSTY 60  
Db 3 EIQLVSGPELKKRGRTYKISCKASGYTFANYGMNMKQAPGKGLKMMGWINTYTGQSTY 62  
QY 61 ADDPKERAFSELETSATTAHLQINNLKNEEDSATYFCARRF---GFAYWGQGLVSVAS 116  
Db 63 AEEFKRPFSELETSATTAHLQINNLKNEEDSATYFCARRF---GFAYWGQGLVSVAS 121  
QY 117 ISSSSSSSSSSSSSSSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLOEPPDGT 176  
Db 122 -SSSSSSSSSSSSSS--SDIWMTQSPKFMSTSVGRVSIKCAASQDVSTAVAWYQKPGQS 178  
QY 177 IKRLIYATSLDGVGPKRFGSGSGSDYSLTSSLESEDFVYVYCLQYALPYPTGGGNTN 236  
Db 179 PKLLIYMTSTHTGTGVPDRFTSGSGSDYTLTSSVQAEALALHYCQGHYRVPTFGGGTK 238  
QY 237 LEIKRAD 243  
Db 239 LEIKRAD 245

RESULT 7

US-08-461-184-8

Sequence 8, Application US/08461184

Patent No. 5631158

GENERAL INFORMATION:

APPLICANT: DORAI, HAIMANTI

APPLICANT: OPPERMAN, HERMANN

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN

TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC

STREET: 45 SOUTH STREET

CITY: HOPKINTON

STATE: MA

COUNTRY: USA

ZIP: 01718

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,184

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/143,498

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: KELLEY, ROBIN D

REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: CRP093

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/248-7000

TELEFAX: 617/248-7100

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 250 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-461-184-8

Query Match 72.7%; Score 914; DB 1; Length 250;  
Best Local Similarity 71.7%; Pred. No. 3.1e-74;  
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

QY 1 EIQLVSGPELKKRGRTYKISCKASGYTFANYGMNMKQAPGKGLKMMGWINTYTGQSTY 60  
Db 3 EIQLVSGPELKKRGRTYKISCKASGYTFANYGMNMKQAPGKGLKMMGWINTYTGQSTY 62  
QY 61 ADDPKERAFSELETSATTAHLQINNLKNEEDSATYFCARRF---GFAYWGQGLVSVAS 116  
Db 63 AEEFKRPFSELETSATTAHLQINNLKNEEDSATYFCARRF---GFAYWGQGLVSVAS 121  
QY 117 ISSSSSSSSSSSSSSSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLOEPPDGT 176  
Db 122 -SSSSSSSSSSSSSS--SDIWMTQSPKFMSTSVGRVSIKCAASQDVSTAVAWYQKPGQS 178  
QY 177 IKRLIYATSLDGVGPKRFGSGSGSDYSLTSSLESEDFVYVYCLQYALPYPTGGGNTN 236  
Db 179 PKLLIYMTSTHTGTGVPDRFTSGSGSDYTLTSSVQAEALALHYCQGHYRVPTFGGGTK 238  
QY 237 LEIKRAD 243  
Db 239 LEIKRAD 245

RESULT 8  
US-08-463-675-8  
Sequence 8, Application US/08463675  
Patent No. 5658763  
GENERAL INFORMATION:

```

; APPLICANT: DORAI, HAIMANTI
; APPLICANT: OPPERMAN, HERMANN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
; TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,675
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/143,498
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-463-675-8

```

```

Query Match      72.7%; Score 914; DB 1; Length 250;
Best Local Similarity 71.7%; Pred. No. 3.1e-74;
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

QY      1 EIQLVQSGBELKPKPEYKISCKASGYTFPTNYGMNWKQAPGKGLKMGWINTNYGQSTY 60
DB      3 EIQLVQSGBELKPKPEYKISCKASGYTFPTNYGMNWKQAPGKGLKMGWINTNYGEPY 62
QY      61 ADFKFRPAFSLSTATTATLHLOINLKNEDSATYFCARF---GPAVYGQGTIVSVAS 116
DB      63 AEFKGRPAFSLSTATTATLHLOINLKNEDSATYFCGRQFITYGGFANMGQGLTVVSA- 121
QY      117 ISSSSGSSSSGSSGSDIQMTQSPSPSLASLGERVSLTCRASODIGNSLTWLQOEPPDGT 176
DB      122 -SSSSGSSSSGSSS--SDIWMQSPKFMSTSVGDVYSISCKASQDVSTAVANYQOKPGQS 178
QY      177 IKRLIYATSSLDGVPKPFSGSRGSDVSLTISLSESEFVYVYCIQVAFIPYTTGGGCTN 236
DB      179 PRLIYMTSTRHTGVDPFTSGSGSDTYLTLTISVQAEIDLALHYCOQHRYRVEYTFGGGTR 238
QY      237 LEIKRAD 243
DB      239 LEIKRAD 245

```

```

RESULT 9
US-08-464-589-8
; Sequence 8, Application US/08464589
; Patent No. 5733782
; GENERAL INFORMATION:
; APPLICANT: DORAI, HAIMANTI
; APPLICANT: OPPERMAN, HERMANN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
; TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA

```

```

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,589
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,498
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-464-589-8

```

```

Query Match      72.7%; Score 914; DB 1; Length 250;
Best Local Similarity 71.7%; Pred. No. 3.1e-74;
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

```

```

QY      1 EIQLVQSGBELKPKPEYKISCKASGYTFPTNYGMNWKQAPGKGLKMGWINTNYGQSTY 60
DB      3 EIQLVQSGBELKPKPEYKISCKASGYTFPTNYGMNWKQAPGKGLKMGWINTNYGEPY 62
QY      61 ADFKFRPAFSLSTATTATLHLOINLKNEDSATYFCARF---GPAVYGQGTIVSVAS 116
DB      63 AEFKGRPAFSLSTATTATLHLOINLKNEDSATYFCGRQFITYGGFANMGQGLTVVSA- 121
QY      117 ISSSSGSSSSGSSGSDIQMTQSPSPSLASLGERVSLTCRASODIGNSLTWLQOEPPDGT 176
DB      122 -SSSSGSSSSGSSS--SDIWMQSPKFMSTSVGDVYSISCKASQDVSTAVANYQOKPGQS 178
QY      177 IKRLIYATSSLDGVPKPFSGSRGSDVSLTISLSESEFVYVYCIQVAFIPYTTGGGCTN 236
DB      179 PRLIYMTSTRHTGVDPFTSGSGSDTYLTLTISVQAEIDLALHYCOQHRYRVEYTFGGGTR 238
QY      237 LEIKRAD 243
DB      239 LEIKRAD 245

```

```

RESULT 10
US-08-461-838-2
; Sequence 2, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Opperman, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: King, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

```

```
ADDRESS: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,838
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-838-2
```

Query Match 72.7%; Score 914; DB 1; Length 250;

Best Local Similarity 71.7%; Pred. No. 3, 1e-74; Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

```
QY 1 EIQLVSGPELKKPGETVTKISCKASGYTFPANYGMNMKQAPGKGLKMGMINITYGOSTY 60
DB 3 EIQLVSGPELKKPGETVTKISCKASGYTFPANYGMNMVQAPGKGLKMGMINITYGOSTY 62
QY 61 ADDFKRPAFSLTSTATTALQINNLRNDSATFYCARF---GPAWGGCTLVSVAS 116
DB 63 AEEFKRPAFSLTSTATTALQINNLRNDSATFYCARF---GPAWGGCTLVSVAS 121
QY 117 ISSSSSSSSSSSSSSSDIOMTQSPSSLSASLGERVSLTCRASODIGNSLTLMOEPPGT 176
DB 122 -SSSSSSSSSSSSSS--SDIWMTQSPKFWSTVGDVRSISCKASQDVSTAVAMTQKPGQS 178
QY 177 IKRLIYATSLDGVKPKFSGSRSGSDYSLTISLSEDFVYYCLQVAFPYTFGGGTN 236
DB 179 PKLLIYMTSTRHTGVDFRTSGSGSDTYLTLLISSVQADLALHYCQGHYRVPTTGGGTN 238
QY 237 LEIKRAD 243
DB 239 LEIKRAD 245
```

RESULT 11  
US-08-461-386-2

```
/ Sequence 2, Application US/08461386
/ Patent No. 5837846
/ GENERAL INFORMATION:
/ APPLICANT: Huston, James S.
/ APPLICANT: Oppermann, Hermann
/ APPLICANT: Houston, L. L.
/ APPLICANT: Ring, David B.
/ TITLE OF INVENTION: Biosynthetic Binding Proteins For
/ TITLE OF INVENTION: Imaging
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Testa, Hurwitz & Thibault/Patent Department
/ STREET: Exchange Place, 53 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
```

```
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,386
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-386-2
```

Query Match 72.7%; Score 914; DB 2; Length 250;

Best Local Similarity 71.7%; Pred. No. 3, 1e-74; Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

```
QY 1 EIQLVSGPELKKPGETVTKISCKASGYTFPANYGMNMKQAPGKGLKMGMINITYGOSTY 60
DB 3 EIQLVSGPELKKPGETVTKISCKASGYTFPANYGMNMVQAPGKGLKMGMINITYGOSTY 62
QY 61 ADDFKRPAFSLTSTATTALQINNLRNDSATFYCARF---GPAWGGCTLVSVAS 116
DB 63 AEEFKRPAFSLTSTATTALQINNLRNDSATFYCARF---GPAWGGCTLVSVAS 121
QY 117 ISSSSSSSSSSSSSSSDIOMTQSPSSLSASLGERVSLTCRASODIGNSLTLMOEPPGT 176
DB 122 -SSSSSSSSSSSSSS--SDIWMTQSPKFWSTVGDVRSISCKASQDVSTAVAMTQKPGQS 178
QY 177 IKRLIYATSLDGVKPKFSGSRSGSDYSLTISLSEDFVYYCLQVAFPYTFGGGTN 236
DB 179 PKLLIYMTSTRHTGVDFRTSGSGSDTYLTLLISSVQADLALHYCQGHYRVPTTGGGTN 238
QY 237 LEIKRAD 243
DB 239 LEIKRAD 245
```

RESULT 12  
US-08-356-786-16

```
/ Sequence 16, Application US/08356786
/ Patent No. 5877305
/ GENERAL INFORMATION:
/ APPLICANT: Huston, James S.
/ APPLICANT: Oppermann, Hermann
/ APPLICANT: Houston, L. L.
/ APPLICANT: Ring, David B.
/ TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
/ TITLE OF INVENTION: Marker
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
/ STREET: Exchange Place, 53 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
```

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,786  
FILING DATE: 06-APR-1995  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/831,967  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fletcher, Edmund R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 622 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-786-16

Query Match 70.8%; Score 891; DB 2; Length 622;  
Best Local Similarity 70.4%; Pred. No. 1,2e-71;  
Matches 174; Conservative 32; Mismatches 33; Indels 8; Gaps 3;

QY 1 ETQLVSGELKPKGETVYKISCKASGYTFYNTGMMVKQAPGKGLKMGIMINTYTGQSTY 60  
DB 3 ETQLVSGELKPKGETVYKISCKASGYTFYNTGMMVKQAPGKGLKMGIMINTYTGQSTY 62  
QY 61 ADFFKRFAPSLSETATTAHLQINNLRNEDSATYFCARF---GFAYWGQGLTVSVAS 116  
DB 63 AEEFGRFAPSLSETATTAHLQINNLRNEDSATYFCARF---GFAYWGQGLTVSVAS 121  
QY 117 ISSSSSSSSSSSSSSSDIQTQSPSSLSASLGERVSLTCRASQDIGNSLTLWQEPDGT 176  
DB 122 -SSSSSSSSSSSS--SDIVMTQSPKFMSTVGDRIKISCKASQDVSTAVANYQKPKGS 178  
QY 177 KRLIYATSLDGVKRPFGSGSDYSLTISLESDFVYVYLCQYALFPYTFGGGTNL 236  
DB 179 KRLIYATSLDGVKRPFGSGSDYSLTISLESDFVYVYLCQYALFPYTFGGGTNL 238  
QY 237 LEIKRAD 243  
DB 239 LEIKRAD 245

RESULT 13  
US-08-488-113B-148  
Sequence 148, Application US/08488113B  
Patent No. 5744580  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B

FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 148:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-148

Query Match 65.7%; Score 827; DB 1; Length 240;  
Best Local Similarity 65.8%; Pred. No. 1.9e-66;  
Matches 160; Conservative 28; Mismatches 49; Indels 6; Gaps 2;

QY 1 ETQLVSGELKPKGETVYKISCKASGYTFYNTGMMVKQAPGKGLKMGIMINTYTGQSTY 60  
DB 1 ETQLVSGGGLVKGSGSVKISCAASGYTFYNTGMMVKQAPGKGLKMGIMINTYTGQSTY 60  
QY 61 ADFFKRFAPSLSETATTAHLQINNLRNEDSATYFCARF---GFAYWGQGLTVSVAS 117  
DB 61 ADSFKRFAPSLSDKRNRYLQINSLRAEDTAVYCTRGRGYMYFVWQGTIVYS--- 117  
QY 118 SSSSSSSSSSSSSSDIQTQSPSSLSASLGERVSLTCRASQDIGNSLTLWQEPDGT 177  
DB 118 SGGGSGGGGSGGSGSDIQTQSPSSLSASVGDVYITCRASQDINSYLSWFOQKPKAP 177  
QY 178 KRLIYATSLDGVKRPFGSGSDYSLTISLESDFVYVYLCQYALFPYTFGGGTNL 237  
DB 178 KRLIYATSLDGVKRPFGSGSDYSLTISLESDFVYVYLCQYALFPYTFGGGTNL 237  
QY 238 EIK 240  
DB 238 EIK 240

RESULT 14  
US-08-477-484B-148  
Sequence 148, Application US/08477484B  
Patent No. 5756699  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago

STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,484B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 148:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-484B-148

Query Match 65.7%; Score 827; DB 1; Length 240;  
Best Local Similarity 65.8%; Pred. No. 1.9e-66;  
Matches 160; Conservative 28; Mismatches 49; Indels 6; Gaps 2;

QY 1 EIQLVOSGPELKKPGETVTKISKASGYTFPANYGMNMWQAQPGKGLKMGWINTYTGOSTY 60  
DB 1 EIQLVOSGGGLVPGGSVIRISCAASGYTTNNGMNVRAQPGKGLMGWINTHTGEPTY 60  
QY 61 ADDPKERFAFSLETATTAHLQINLRNEDSATYFCARR---FGPAYWGQGLTVSVASAI 117  
DB 61 ADSFKGRFTFSLDDSKRTAYLQINSLRAEDTAVYFCTRRGYDWYFDVWGQGLTVSV--- 117  
QY 118 SSSSGSSSSSSSGSDIQMTOSPSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTI 177  
DB 118 SGGGGSGGGSGGGSDIQMTOSPSLSASVGDRTVITCRASQDINSYLSWFOQKPKAP 177  
QY 178 KRLIYATSSLDGCVPRFRSGRSRGSQDYSLTISLSSEDFVYVYCCLOYAIFPTTGGGNTL 237  
DB 178 KTLIYRANLBSGVPRFRSGRSRGSQDYTLTISLSQYEDFGIYCCQGYDSDSPWTFGGGNTL 237  
QY 238 EIK 240  
DB 238 EMK 240

RESULT 15  
US-08-646-360-148  
Sequence 148, Application US/08646360  
Patent No. 5837491  
GENERAL INFORMATION:

APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-9155  
TELEFAX: 650 388-1248  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 148:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-360-148

Query Match 65.7%; Score 827; DB 2; Length 240;  
Best Local Similarity 65.8%; Pred. No. 1.9e-66;  
Matches 160; Conservative 28; Mismatches 49; Indels 6; Gaps 2;

QY 1 EIQLVOSGPELKKPGETVTKISKASGYTFPANYGMNMWQAQPGKGLKMGWINTYTGOSTY 60  
DB 1 EIQLVOSGGGLVPGGSVIRISCAASGYTTNNGMNVRAQPGKGLMGWINTHTGEPTY 60  
QY 61 ADDPKERFAFSLETATTAHLQINLRNEDSATYFCARR---FGPAYWGQGLTVSVASAI 117  
DB 61 ADSFKGRFTFSLDDSKRTAYLQINSLRAEDTAVYFCTRRGYDWYFDVWGQGLTVSV--- 117  
QY 118 SSSSGSSSSSGSDIQMTOSPSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTI 177  
DB 118 SGGGGSGGGSGGGSDIQMTOSPSLSASVGDRTVITCRASQDINSYLSWFOQKPKAP 177  
QY 178 KRLIYATSSLDGCVPRFRSGRSRGSQDYSLTISLSSEDFVYVYCCLOYAIFPTTGGGNTL 237  
DB 178 KTLIYRANLBSGVPRFRSGRSRGSQDYTLTISLSQYEDFGIYCCQGYDSDSPWTFGGGNTL 237



Oy 238 EIK 240  
 Db 238 EIK 240

Search completed: April 4, 2005, 16:00:49  
 Job time : 129.217 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 15:19:49 ; Search time 21.9649 seconds  
(without alignments)  
193.690 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_157\_167

Sequence: 1 RASQDIGNSLT 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp19808:\*\n2: geneseqp19908:\*\n3: geneseqp20008:\*\n4: geneseqp20018:\*\n5: geneseqp20028:\*\n6: geneseqp20038:\*\n7: geneseqp20048:\*\n8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	107	3	AAV90824
2	53	100.0	243	2	AAW02280
3	53	100.0	243	2	AAW53170
4	53	100.0	243	2	AAW80424
5	53	100.0	243	7	ABW00716
6	53	100.0	246	2	AAW39569
7	53	100.0	267	4	AAU04944
8	53	100.0	409	4	AAU04945
9	53	100.0	534	2	AAW39571
10	48	90.6	109	2	AAW06388
11	45	84.9	112	5	AAW50879
12	43	81.1	11	8	ADM78135
13	43	81.1	90	2	AAW80078
14	43	81.1	92	2	AAW95480
15	43	81.1	92	2	AAW95476
16	43	81.1	107	2	AAW78972
17	43	81.1	107	2	AAW79247
18	43	81.1	107	2	AAW79250
19	43	81.1	107	2	AAW27121
20	43	81.1	108	2	AAW21310
21	43	81.1	108	8	AD126702
22	43	81.1	109	2	AAW18271
23	43	81.1	109	2	AAW85910
24	43	81.1	109	4	AAW65862
25	43	81.1	109	5	ABP51796

26	43	81.1	109	6	ABU58877	ABU58877	Anti-prio
27	43	81.1	109	8	ADJ10235	ADJ10235	Murine an
28	43	81.1	130	8	ADJ26651	ADJ26651	Human ant
29	43	81.1	144	8	ADJ57086	ADJ57086	3G4 anti b
30	43	81.1	153	8	ADJ57089	ADJ57089	3G4-2BVL-
31	43	81.1	252	5	AAU72863	AAU72863	P4-14 61n
32	43	81.1	257	5	AAU72869	AAU72869	P5-11 61n
33	43	81.1	499	5	AAU72872	AAU72872	3B10xP4-1
34	42	79.2	11	2	AAW23433	AAW23433	CDR-1 of
35	42	79.2	108	2	AAW23439	AAW23439	Modified
36	42	79.2	108	2	AAW23440	AAW23440	Modified
37	42	79.2	108	2	AAW23442	AAW23442	hm12 11gh
38	42	79.2	108	2	AAW23436	AAW23436	hm12 11gh
39	42	79.2	109	2	AAW06382	AAW06382	Humanised
40	41	77.4	106	5	ABG76546	ABG76546	HCV E1 an
41	39	73.6	11	3	AAW52526	AAW52526	3D6 11gh
42	39	73.6	11	3	AAW44589	AAW44589	Mouse ant
43	39	73.6	11	8	ADO60477	ADO60477	Mouse ant
44	39	73.6	95	2	AAW18269	AAW18269	Prp 81 11
45	39	73.6	95	2	AAW85908	AAW85908	Prp 81 11

## ALIGNMENTS

RESULT 1  
AAV90824  
ID AAV90824 standard; protein; 107 AA.

AC AAV90824;

DT 29-AUG-2000 (first entry)

DE 520C9 hybridoma VL domain SEQ ID NO:26.

KW Antigen binding site; immunoglobulin; cancer antigen; immunological;

KW antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;

KW specific binding assay; affinity purification; drug targeting;

KW toxin targeting; imaging; genetic; therapeutic.

OS Homo sapiens.

XX US6054561-A.

XX 25-APR-2000.

XX 07-JUN-1995; 95US-00483749.

XX 08-FEB-1984; 84US-00577976.

XX 11-JAN-1985; 85US-00690750.

XX 21-MAR-1986; 86US-00842476.

XX 08-MAY-1988; 88US-00190778.

XX 11-AUG-1994; 94US-00288981.

XX (CHTR ) CHIRON CORP.

XX Ring DB;

XX WPI; 2000-336508/29.

XX N-PEDB; AAA38908.

XX Monoclonal antibody capable of binding to human breast cancer antigen

XX useful for affinity purification, drug or toxin targeting, imaging, and

XX treating cancer.

XX Disclosure: Fig 13; 57pp; English.

CC The present invention describes a monoclonal antibody (Mab) (I) that

CC binds to a human breast cancer antigen that is also bound by Mab 45C11

CC and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also

CC described is a hybridoma that produces (I). (I) is useful in specific

CC binding assays, affinity purification, drug or toxin targeting, imaging,

CC and genetic or immunological therapeutics for various cancers. The

CC present sequence represents a VL domain derived from a 520C9 hybridoma,  
CC which is used in the exemplification of the present invention  
XX  
SQ Sequence 107 AA;

Query Match 100.0%; Score 53; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11  
DB 24 RASODIGNSLT 34

RESULT 2  
AAW02280  
ID AAW02280 standard; protein; 243 AA.

AC AAW02280;

DT 25-MAR-2003 (revised)

DT 29-OCT-1996 (first entry)

DE 520C9 anti-c-erbB-2 two single chain Fv construct.

KW 520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sfv;  
KW construct; polypeptide linker; C-terminal amino acid sequence;  
KW in vivo imaging; drug targeting experiment; homodimer; increased;  
KW binding avidity; tissue retention time.

OS Homo sapiens.

PH Key Location/Qualifiers  
FT Peptide 118..133  
/label= linker

PN US5534254-A.

PD 09-JUL-1996.

PF 07-OCT-1993; 93US-00133804.

PR 06-FEB-1992; 92US-00831967.

PA (CHIR ) CHIRON CORP.

PA (CREA-) CREATIVE BIOMOLECULES INC.

PI Oppermann H, Ring DB, Huston JS, Houston LL;

DR WPI; 1996-333194/33.

DR N-PSDB; AAT36880.

CC Compens. contg. antigen-targeting antibody fragment constructs -  
CC comprising dimer of single-chain Fv fragments.

PS Example 1; Col 33-36; 30pp; English.

XX Variable heavy (VH) and variable light (VL) genes were cloned from a  
CC 520C9 hybridoma cDNA library, using probes directed toward the antibody  
CC constant and joining regions. A two single chain Fv (sfv) gene was  
CC constructed by connecting the VH and VL genes with a Ser rich polypeptide  
CC linker. The resulting 520C9 two sfv gene, which encodes the present  
CC sequence, was inserted into an expression vector, transformed into E.  
CC coli, and protein expression induced by the addn. of IPTG to the culture  
CC medium. A compens. comprising a carrier and the 2 sfv protein prod. can be  
CC used for in vivo imaging, and drug targeting experiments. The 2 sfv  
CC protein prod. is a homodimer, in which both fragments target the same  
CC antigen, therefore giving greater binding avidity and longer tissue  
CC retention times, compared to individual sfv protein prod. fragments.  
CC (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 243 AA;

Query Match 100.0%; Score 53; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.057;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11  
DB 157 RASODIGNSLT 167

RESULT 3  
AAW53170  
ID AAW53170 standard; protein; 243 AA.

AC AAW53170;

DT 16-JUL-1998 (first entry)

DE 520C9 anti-c-erbB-2 sfv' dimeric construct protein sequence.

KW Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer; c-erbB-2;  
KW tumour; diagnosis; ss.

OS Synthetic.

OS Mus sp.

PN US5753204-A.

PD 19-MAY-1998.

PF 05-JUN-1995; 95US-00461838.

PR 06-FEB-1992; 92US-00831967.

PR 07-OCT-1993; 93US-00133804.

PA (CHIR ) CHIRON CORP.  
PA (CREA-) CREATIVE BIOMOLECULES INC.

PI Oppermann H, Ring DB, Huston JS, Houston LL;

DR WPI; 1998-311318/27.

DR N-PSDB; AAV21798.

CC Imaging of antigens in vivo - using dimers of single-chain antibody Fv  
CC fragments.

PS Example 1; Col 33-36; 30pp; English.

XX This represents the protein sequence of a 520C9 sfv' (single chain Fv)  
CC construct. This was constructed by connecting the VH and VL genes with a  
CC DNA sequence encoding a Serine rich linker. 520C9 is a monoclonal  
CC antibody useful in targeting c-erbB-2 antigen. This dimeric construct can  
CC be used in the methods of invention of imaging a preselected antigen  
CC expressed in a mammal. The methods are used in magnetic resonance imaging  
CC of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic  
CC constructs have enhanced properties as in vivo targeting agents in  
CC comparison with intact monoclonal antibodies or their Fab fragments. The  
CC dimeric constructs permit the in vivo targeting of an epitope on an  
CC antigen with greater apparent avidity, including greater tumour  
CC specificity, tumour localisation and tumour retention properties than  
CC that of the Fab fragment having the same CDRs as the construct  
XX

SQ Sequence 243 AA;

Query Match 100.0%; Score 53; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.057;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11  
DB 157 RASODIGNSLT 167

RESULT 4

AAW80424  
ID AAW80424 standard; protein; 243 AA.  
XX  
AC AAW80424;  
XX  
DT 28-JAN-1999 (first entry)  
XX  
DE 520C9 gFv sequence.  
XX  
XX 520C9 gFv; antigen; tumour cell; antibody 520C9; targeted delivery;  
KM antigen-expressing cell.  
XX  
OS Synthetic.  
XX  
PN US5837846-A.  
PD 17-NOV-1998.  
XX  
PF 05-JUN-1995; 95US-00461386.  
XX  
PR 06-FEB-1992; 92US-00831967.  
XX  
PR 07-OCT-1993; 93US-00133804.  
XX  
PA (CREA-) CREATIVE BIOMOLECULES INC.  
XX (CHIR ) CHIRON CORP.  
PI Oppermann H, Houston LL, Huston JS, Ring DB;  
XX  
XX WPI; 1999-023541/02.  
DR N-PSDB; AAW63399.  
XX  
XX Nucleic acid encoding single-chain Fv fragment specific for antigens -  
PT and having C-terminal tail for crosslinking to form dimer with improved  
PT pharmacokinetic properties, used to deliver drugs and imaging agents,  
XX especially to tumours.  
XX  
XX Example 1; Col 35-36; 29pp; English.  
XX  
XX The present sequence represents an antibody 520C9 gFv. Variable heavy and  
CC light sequences of antibody 7520C9 are connected, together with a serine  
CC linker, to produce the present single chain Fv gene. The present sequence  
CC exemplifies the invention. Dimers of the single chain Fv are used for  
CC targeted delivery of drugs or imaging agents (e.g. cytotoxins, produgs  
CC or 99m-technetium) to antigen-expressing cells, particularly for  
CC treatment or diagnosis of tumours (especially of ovary or breast)  
XX  
SQ Sequence 243 AA;  
XX  
Query Match 100.0%; Score 53; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.057;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RASODIGNSLT 11  
DB 157 RASODIGNSLT 167  
XX  
RESULT 5  
ABW00716  
ID ABW00716 standard; protein; 243 AA.  
XX  
AC ABW00716;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE 520C9 gFv protein.  
XX  
XX Cell proliferation; cytotoxic agent; drug targeting; single-chain Fv;  
KM gFv.  
XX  
OS Unidentified.  
XX  
PN US2002168375-A1.  
XX

XX  
PD 14-NOV-2002.  
XX  
PF 21-JUN-2001; 2001US-00887853.  
XX  
XX 06-FEB-1992; 92US-00831967.  
XX  
PR 07-OCT-1993; 93US-00133804.  
XX  
PR 05-JUN-1995; 95US-00462641.  
XX  
PR 26-APR-2000; 2000US-00558741.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
XX Huston JS, Houston LL, Ring DB, Oppermann H;  
PI WPI; 2003-765156/72.  
XX  
DR N-PSDB; AAD61485.  
XX  
XX Novel binding protein formulation for targeting epitope on antigen in  
PT mammal, comprising dimeric biosynthetic construct having conformation  
PT permitting binding of antigen by binding site of each polypeptide chain.  
XX  
XX Example 1; Page 19-20; 30pp; English.  
XX  
XX The invention relates to a binding protein formulation for targeting an  
CC epitope on an antigen expressed in mammal. The formulation comprises of  
CC dimeric biosynthetic construct having conformation permitting binding of  
CC antigen by binding site of each polypeptide chain. The invention is  
CC useful for imaging a preselected antigen in a mammal expressing the  
CC antigen. It is also useful for targeting drugs that inhibits cell  
CC proliferation and cytotoxic agents that kill cells. The present sequence  
CC is 520C9 gFv protein. This sequence is used in the exemplification of the  
XX invention  
XX  
SQ Sequence 243 AA;  
XX  
Query Match 100.0%; Score 53; DB 7; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.057;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RASODIGNSLT 11  
DB 157 RASODIGNSLT 167  
XX  
RESULT 6  
AAR39569  
ID AAR39569 standard; protein; 246 AA.  
XX  
AC AAR39569;  
XX  
DT 25-MAR-2003 (revised)  
XX  
DT 07-FEB-1994 (first entry)  
XX  
DE Sequence of 520C9 gFv protein.  
XX  
XX Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;  
KM biosynthetic single polypeptide chain binding site; sb.  
XX  
OS Synthetic.  
XX  
PN WO9316185-A2.  
XX  
PD 19-AUG-1993.  
XX  
PF 05-FEB-1993; 93WO-US001055.  
XX  
PR 06-FEB-1992; 92US-00831967.  
XX  
XX (CREA-) CREATIVE BIOMOLECULES INC.  
PA (CETU ) CETUS ONCOLOGY CORP.  
XX  
XX Huston JS, Houston LL, Ring DB, Oppermann H;  
XX

Query Match	100.0%	Score 53;	DB 2;	Length 246;
Best Local Similarity	100.0%;	Pred. No. 0.057;		
Matches 11; Conservative	0;	Mismatches	0;	Gaps 0;

RESULT 7  
AAU04944  
ID AU04944 standard; protein; 267 AA.

DE Humanised anti-p185 single chain antibody, 520C9H.  
XX  
KM Humanised, antibody, p185, 520C9H; interleukin-2, IL-2; immunocjugate;  
KW cancer; tumour; adenocarcinoma.

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72. .88	

	/note= "Complementary determining region"
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FT	.121
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	/label= CDR
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Pentide	

Region	Linker
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FT	/note= "Links the heavy chain to the light chain"
FT	176 196

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FT      /label= CDR
FT      /note= "Complementarity determining region"
FT      202      308
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/label= CDR
/notes= "Complementarity determining region"

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FT /label= CDR
FT /note= "Complementarity determining region"
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PF	19-JAN-2001; 2001WO-US001919.
XX	
PR	20-JAN-2000; 2000US-0177258P.

PA (CHIR ) CHIRON CORP.  
PA (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC  
PA (HAMI-) HAMILTON REGIONAL CANCER CENT.

XX WPI; 2001-451904/48.  
DR N-PSDB; AAS09507.  
DR

PT Novel immunoconjugate useful for inhibiting tumor cell growth in vivo  
PT comprises a humanized anti-p185 antibody linked to an interleukin-2  
PI polypeptide.  
PS  
XX Claim 7; fig 9; 74pp; English.

CC The sequence represents a humanised anti-p185 single chain antibody which  
CC is linked to a human interleukin-2 (IL-2) molecule to make a fusion  
CC protein. The fusion protein (or immunocjugate) is used to inhibit the  
CC growth of tumours or cancers particularly those characterised by  
CC overexpression of p185 e.g. human adenocarcinomas and malignant and/or  
CC benign tumours of the breast, renal system, salivary gland,  
CC gastrointestinal tract or gastric tumours. (Updated on 06-AUG-2003 to  
CC correct OS field.)

SQ Sequence 267 AA;

Query Match	100.0%	Score 53;	DB 4;	Length 267;
Best Local Similarity	100.0%;	Pred. No. 0.063;		
Matches 11; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

```
QY      1 RASQDIGNSLT 11
Db      176 RASQDIGNSLT 186
```

RESULT 8  
AAU04945  
ID AAU04945 standard; protein; 409 AA.

DT	06-AUG-2003	(revised)
DT	24-OCT-2001	(first entry)

DE Humanised anti-p185 antibody/IL-2 fusion protein.

KM Humanised; antibody; p135; 520C9H; interleukin-2; IL-2; immunoconjugate;  
KM cancer; tumour; adenocarcinoma; fusion protein.

OS Homo sapiens.

OS	Synthetic.
OS	Chimeric.

FH	Key	Location/Qualifiers
FT	Peptide	1. .22

FT	/label= signal_peptide
1	1
2	1
3	1
4	1
5	1
6	1
7	1
8	1
9	1
10	1
11	1
12	1
13	1
14	1
15	1
16	1
17	1
18	1
19	1
20	1
21	1
22	1
23	1
24	1
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26	1
27	1
28	1
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30	1
31	1
32	1
33	1
34	1
35	1
36	1
37	1
38	1
39	1
40	1
41	1
42	1
43	1
44	1
45	1
46	1
47	1
48	1
49	1
50	1
51	1
52	1
53	1
54	1
55	1
56	1
57	1
58	1
59	1
60	1
61	1
62	1
63	1
64	1
65	1
66	1
67	1
68	1
69	1
70	1
71	1
72	1
73	1
74	1
75	1
76	1
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83	1
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87	1
88	1
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90	1
91	1
92	1
93	1
94	1
95	1
96	1
97	1
98	1
99	1
100	1

Protein	23.409
FT	
EM	

FT	Protein
FT	

```

11  PROCERN 23. .239
12  /label= Humanised antibody 520C9H
13  FT

```

Region

```

FT FT /label= CDR
FT FT /note= "Complementarity determining region"
FT FT Region
FT FT /label=.88
FT FT /note= "Complementarity determining region"
FT FT Region
FT FT /label=.126
FT FT /note= "Complementarity determining region"
FT FT /label=.123
FT FT /note= "Encoded by GGG"
FT FT /label=.152
FT FT /note= "Synthetic peptide linker"
FT FT /note= "Links the heavy chain to the light chain"
FT FT Region
FT FT /label= CDR
FT FT /note= "Complementarity determining region"
FT FT /label=.208
FT FT /note= "Complementarity determining region"
FT FT Region
FT FT /label=.249
FT FT /label= CDR
FT FT /note= "Complementarity determining region"
FT FT Peptide
FT FT /label=.261
FT FT /note= "Complementarity determining region"
FT FT /label= "Synthetic linker peptide"
FT FT /note= "Links the antibody to the IL-2 molecule"
FT FT Protein
FT FT /label=.277
FT FT /label= IL_2
FT FT /note= "Encode by ACA"
FT FT Misc-difference
FT FT /label= 406
FT FT /note= "Encode by ACA"
FT FT WO20015354-A2.
FT FT 26-JUL-2001.
FT FT 19-JAN-2001; 2001WO-US001919.
FT FT 20-JAN-2000; 2000US-0177258P.
FT FT (CHIR ) CHIRON CORP.
FT FT (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.
FT FT (HAMI-) HAMILTON REGIONAL CANCER CENT.
FT FT Austin R, Kwok CS, Ring DB;
FT FT WPI; 2001-451904/48.
FT FT N-PSDB; AAS09508.
FT FT Novel immun conjugate useful for inhibiting tumor cell growth in vivo
FT FT comprises a humanized anti-p185 antibody linked to an Interleukin-2
FT FT polypeptide.
FT FT Claim 13; Fig 11; 74pp; English.
FT FT The sequence represents a humanised anti-p185 (520c9) single chain
FT FT antibody/human interleukin-2 (IL-2) fusion protein. The fusion protein
FT FT (or immun conjugate) is used to inhibit the growth of tumours or cancers
FT FT particularly those characterised by overexpression of p185 e.g. human
FT FT adenocarcinomas and malignant and/or benign tumours of the breast, renal
FT FT system, salivary gland, gastrointestinal tract or gastric tumours.
FT FT (Updated on 06-AUG-2003 to correct OS field.)
FT FT Sequence 409 AA;
SQ
Query Match 100.0%; Score 53; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASODIGNSLT 11
DB 176 RASODIGNSLT 186

```

```

AAR39571
ID AAR39571 standard; protein; 534 AA.
XX
XX AAR39571;
AC
XX 25-MAR-2003 (revised)
DT 07-FEB-1994 (first entry)
XX
XX Sequence of G-FIT.
DE
XX Tumour antigen; c-erbB-2; G-FIT.
XX
XX Synthetic.
OS
XX WO9316185-A2.
XX 19-AUG-1993.
XX
XX 05-FEB-1993; 93WO-US001055.
XX
XX 06-FEB-1992; 92US-00831967.
XX
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX (CERTU ) CERTUS ONCOLOGY CORP.
XX
XX Huston JS, Houston LL, Ring DB, Oppermann H;
XX
XX WPI; 1993-272889/34.
XX
XX N-PSDB; AAQ46086.
XX
XX New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for
XX imaging or treating breast or ovarian cancer etc.
XX
XX Example; Page 65-68; 87pp; English.
XX
XX c-erbB-2 refers to a protein antigen expressed on the surface of tumour
XX cells, such as breast and ovarian tumour cells, which is an approx.
XX 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about
XX 5.3 (see AAQ46083, AAR39568). (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
XX Sequence 534 AA;
SQ
Query Match 100.0%; Score 53; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASODIGNSLT 11
DB 448 RASODIGNSLT 458

```

```

RESULT 10
AAY06388
ID AAY06388 standard; protein; 109 AA.
XX
XX AAY06388;
AC
XX
XX 06-SEP-1999 (first entry)
DT
XX
XX Humanised LM609 antibody VL domain.
DE
XX
XX Humanised antibody; antibody humanisation; antibody engineering; LM609;
XX monoclonal antibody; complementarity determining region; CDR grafting;
XX mouse; human; integrin; apoptosis; angiogenesis; cancer; therapy;
XX diagnosis.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..2
XX /note= "vector-encoded residues"

```

```

FT Region 24. .34
FT /note= "CDR1"
FT Region 50. .56
FT /note= "CDR2"
FT Region 89. .97
FT /note= "CDR3"
XX
XX WO9929888-A1.
XX
XX 17-JUN-1999.
XX
XX 04-DEC-1998; 98WO-US025828.
XX
XX 05-DEC-1997; 97US-00986016.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
XX
XX WPI; 1999-394979/33.
XX
XX Production of humanized mouse monoclonal antibodies.
XX
XX Disclosure; Page 52; 55pp; English.
XX
XX This sequence represents the light chain variable region of a humanised
XX LM609 antibody. LM609 is directed to human integrin alpha-v-beta-3. It
XX selectively promotes apoptosis of vascular cells that have been
XX stimulated to undergo angiogenesis, making it a tool for cancer diagnosis
XX and therapy. The invention provides humanised antibodies, especially
XX humanised LM609. In such humanized antibodies, a light chain CDR from a
XX mouse antibody such as LM609 is grafted onto a human light chain, and a
XX heavy chain CDR from a mouse antibody is grafted onto a human antibody
XX having the desired specificity is selected. By preserving the original
XX CDR sequences such as the HCDR3 and LCDR3 sequences of LM609 (see
XX AA05371-72), the humanisation strategy ensures epitope conservation
XX
XX Sequence 109 AA;
XX
XX Query Match 90.6%; Score 48; DB 2; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 0.23;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RASODIGNSL 10
XX |||||
XX 24 RASODIGNSL 33
XX
XX RESULT 11
XX AAM50879
XX ID AAM50879 standard; protein; 112 AA.
XX
XX AC AAM50879;
XX
XX DT 07-MAY-2002 (first entry)
XX
XX Anti-bovine prion protein peptide antibody light chain.
XX
XX Prion; prion protein; PrP; PrPc; PrPSc; antibody; Fab; mouse; ungulate;
XX infection; bovine spongiform encephalopathy; BSE; diagnosis; therapy.
XX
XX Mus musculus.
XX
XX WO200210335-A2.
XX
XX 07-FEB-2002.
XX
XX 17-JUL-2001; 2001WO-US022648.
XX
XX 27-JUL-2000; 2000US-00627218.
XX
XX (REGC ) UNITV CALIFORNIA.

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PA (SCRI ) SCRIPPS RES INST.
XX
XX Prusiner SB, Safar J, Williamson AR, Burton DR;
XX
XX WPI; 2002-195957/25.
XX
XX Novel antibody useful for detecting infectious prions, particularly
XX pathogenic scrapie isoform of the prion protein, PrPSc in an ungulate,
XX especially cow, binds to native ungulate prion protein C in situ.
XX
XX Example 1; Page 41; 63pp; English.
XX
XX The present sequence is that of the light chain of a recombinant Fab
XX antibody fragment (Clone P) that binds tightly to denatured bovine PrPsc
XX but not to the native conformation of the same protein in CD10 formatted
XX ELISA. The presence of PrPsc in tissues of humans or animals is
XX indicative of prion infection. The Fab was generated against the 96-105
XX region of bovine prion protein (PrP). Clone P binds to an epitope (see
XX AAM50886-87) that is present in all ungulate PrP sequences, including
XX bovine, and also in other species such as human, sheep and mouse. The P
XX recombinant antibody fragments (Fabs) were isolated from mouse CDNA and
XX cloned into a vector that expressed human-mouse chimeric Fabs in
XX Escherichia coli. The purified Fabs were labeled with Europium, giving an
XX Fab designated Eu-(HuM)Fab P. This is an example of antibodies of the
XX invention that specifically bind with a high degree of binding affinity
XX to a native ungulate PrPc in situ and/or a denatured ungulate PrPsc, but
XX not to a native ungulate PrPsc in situ. The antibodies may specifically
XX bind to epitopes of PrPc of a specific species of animal or to 1 or more
XX types of PrPc proteins from 1 or more species of ungulates. The
XX antibodies are useful for the detection of prion infection in ungulates,
XX particularly cattle. A fast, efficient, cost-effective assay is achieved.
XX The assay can be used to screen for the presence of PrPsc in products
XX such as pharmaceuticals (derived from natural sources), food, cosmetics
XX etc. The antibodies can be used with a compound that denatures PrPsc
XX thereby providing a means of differentiating levels of PrPc and
XX PrPc+PrPSc in a sample. The invention also provides a therapeutic
XX antibody which prevents or treats prion disease in ungulates, and
XX specifically in cattle, and a means for certifying certain products as
XX being prion free
XX
XX Sequence 112 AA;
XX
XX Query Match 84.9%; Score 45; DB 5; Length 112;
XX Best Local Similarity 90.0%; Pred. No. 0.9;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RASODIGNSL 10
XX |||||
XX 24 RASODIGNSL 33
XX
XX RESULT 12
XX ADM78135
XX ID ADM78135 standard; peptide; 11 AA.
XX
XX AC ADM78135;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX Human SUB3-86 antibody variable light chain CDR1 peptide region.
XX
XX Monoclonal antibody; adenylate kinase isozyme 3;
XX complementarity determining region; CDR; heart disease; marker AK3;
XX biochemical; human; variable; light chain.
XX
XX Homo sapiens.
XX
XX WO2004029094-A1.
XX
XX 08-APR-2004.
XX
XX 27-SEP-2003; 2003WO-KR001979.
XX

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PR 28-SEP-2002; 2002KR-00059211.
XX
PA (KIMH/) KIM H.
XX
PI Kim H;
XX
DR WPI; 2004-316088/29.
XX
PT New monoclonal antibody specific to human mitochondrial adenylate kinase
PT isozyme 3, useful for preparing a composition for detecting a heart
PT disease marker AK3.
XX
PS Claim 1; SEQ ID NO 98; 126pp; English.
XX
CC The invention relates to a novel monoclonal antibody specific to
CC adenylylate kinase isozyme 3, comprising 4 or more of 6 complementarily
CC determining regions (CDRs) of a sequence having 6-18 amino acids. The
CC invention further relates to: a composition comprising the monoclonal
CC antibody for detecting a heart disease marker AK3; a kit comprising the
CC monoclonal antibody for the diagnosis of heart disease; and a method of
CC detecting a heart disease marker AK3. The monoclonal antibody is useful
CC for preparing a composition for detecting a heart disease marker AK3. The
CC monoclonal antibody reduces false positive results of the conventional
CC biochemical markers. This sequence represents a human antibody variable
CC light chain CDR peptide region of the invention.
XX
SQ Sequence 11 AA;

Query Match      81.1%; Score 43; DB 8; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
DB 1 RASQDIGSSL 10

RESULT 13
AAR80078
ID AAR80078 standard; protein; 90 AA.
XX
AC AAR80078;
XX
DT 22-MAY-1996 (first entry)
XX
DE Mouse derived light chain RT3 phage antibody pattern A.
XX
KW Light chain; RT3; murine; catalytic antibody; bacteriophage; pattern A.
XX
OS Mus musculus.
XX
PH Location/Qualifiers
PT 1..15
PT /note= "framework region 1"
PT 16..26
PT /note= "complementarity determining region 1"
PT 27..40
PT /note= "framework region 2"
PT 41..47
PT /note= "complementarity determining region 2"
PT 48..78
PT /note= "framework region 3"
PT 79..88
PT /note= "complementarity determining region 3"
PT 89..90
PT /note= "framework region 4 N-terminal fragment"
XX
PN W09527045-A1.
XX
PD 12-OCT-1995.
XX
PF 30-MAR-1994; 94WO-US003420.
XX
```

```
PR 30-MAR-1994; 94WO-US003420.
XX
PA (IGEN-) IGEN INC.
XX
PI Smith RG, Mc Cafferty J, Chiswell D, Darsley MJ, Fitzgerald K;
PI Kenten JH, Martin MT, Tiltmae RC, Williams RO;
XX
DR WPI; 1995-358624/46.
XX
DR N-PSDB; AAT04625.
XX
PT Production of catalytic antibodies displayed on phage - by generating a
PT gene library of antibody-derived domains and expressing it in phage
PT vectors.
XX
PS Disclosure; Fig 9; 133pp; English.
XX
CC AAT04625 encodes AAR80078 mouse derived light chain RT3 phage antibody.
CC The DNA was used in the prepn. of catalytic antibody (CA) producing
CC bacteriophage. The CAs can be used to activate/deactivate a biological
CC function in an animal by enhancing the rate of cleavage, or formation of
CC a specific bond within a mol. in vivo
XX
SQ Sequence 90 AA;

Query Match      81.1%; Score 43; DB 2; Length 90;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
DB 16 RASQDIGSSL 25

RESULT 14
AAW95480
ID AAW95480 standard; protein; 92 AA.
XX
AC AAW95480;
XX
DT 29-MAR-1999 (first entry)
XX
DE Mouse derived RT3 phage antibody light chain pattern C genetic sequence.
XX
KW Catalytic; antibody; phage display; immunising; phage expression vector;
KW produg; scFV.
XX
OS Mus sp.
XX
PN US5855885-A.
XX
PD 05-JAN-1999.
XX
PF 14-JUL-1994; 94US-00273146.
XX
PR 22-JAN-1993; 93US-00007684.
XX
PA (MCCA/) MCCAFFERTY J.
PA (CHIS/) CHISWELL D.
PA (DARS/) DARSLEY M J.
PA (TITM/) TITMAS R C.
PA (MART/) MARTIN M T.
PA (KENT/) KENTEN J H.
PA (SWIT/) SMITH R.
PA (FITZ/) FITZGERALD K.
PA (WILL/) WILLIAMS R O.
XX
PI Fitzgerald K, Darsley MJ, Williams RO, Smith R, Martin MT;
PI Kenten JH, Chiswell D, McCafferty J, Tiltmae RC;
XX
DR WPI; 1999-105036/09.
XX
DR N-PSDB; AAX00879.
XX
PT Production of catalytic antibodies displayed on bacteriophages -
```

```

PR  comprises generating a gene library of antibody-derived domains inserting
PT  coding into a phage expression vector and isolating the catalytic
PT  antibodies.
XX
PS  Example 4; Fig 11; 117pp; English.
XX
CC  The invention relates to methods for producing catalytic antibodies
CC  displayed on a phage. The method comprises: (a) generating a gene library
CC  of antibody-derived domains; (b) inserting coding for the domains into a
CC  phage expression vector; and (c) isolating the catalytic antibodies. The
CC  phage expression vector incorporates a histidine peptide in tandem with a
CC  myc peptide. The catalytic antibodies can be isolated by preparing an
CC  antigen, optionally immunising an animal with the antigen; generating a
CC  library of VH and VL domains from the immunised animal; cloning the VH
CC  and VL domains into a phage expression vector to generate phage display
CC  antibodies; selecting phage display antibodies which bind specifically to
CC  the antigen; screening the selected phage display antibodies for
CC  catalytic activity to substrate; and isolating the catalytic antibodies,
CC  where the phage expression vector incorporates a histidine peptide in
CC  tandem with a myc peptide. The processes are used to produce catalytic
CC  antibodies, which can be used for in vivo activation of a prodrg. The
CC  present sequence represents a genetic sequence of light chain PCR pattern
CC  C from mouse derived RT3 phage antibodies
XX
SQ  Sequence 92 AA;
XX
Query Match      81.1%; Score 43; DB 2; Length 92;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY  1 RASODIGNSL 10
    |||||:|
DB  16 RASQDIGSSL 25
XX
RESULT 15
AAW95476
ID  AAW95476 standard; protein; 92 AA.
XX
AC  AAW95476;
XX
DT  29-MAR-1999 (first entry)
XX
DE  Mouse derived RT3 phage antibody light chain pattern A genetic sequence.
XX
KM  Catalytic; antibody; phage display; immunising; phage expression vector;
XX  prodrg; scFV.
XX
OS  Mus sp.
XX
PN  US5855885-A.
XX
PD  05-JAN-1999.
XX
PF  14-JUL-1994; 94US-00273146.
XX
PR  22-JAN-1993; 93US-00007684.
XX
PA  (MCCA/) MCCAFERTY J.
PA  (CHIS/) CHISWELL D.
PA  (DARS/) DARSLEY M J.
PA  (TITM/) TITMAS R C.
PA  (MART/) MARTIN M T.
PA  (KENT/) KENTEN J H.
PA  (SMIT/) SMITH R.
PA  (FITZ/) FITZGERALD K.
PA  (WILL/) WILLIAMS R O.
XX
PI  Fitzgerald K, Darsley MJ, Williams RO, Smith R, Martin MT;
PI  Kenten JH, Chiswell D, Mccafferty J, Titmas RC;
XX
WPI: 1999-105036/09.
DR  N-PSDB; AAX00875.

```

```

XX  Production of catalytic antibodies displayed on bacteriophages -
PT  comprises generating a gene library of antibody-derived domains inserting
PT  coding into a phage expression vector and isolating the catalytic
PT  antibodies.
XX
PS  Example 4; Fig 9A-F; 117pp; English.
XX
CC  The invention relates to methods for producing catalytic antibodies
CC  displayed on a phage. The method comprises: (a) generating a gene library
CC  of antibody-derived domains; (b) inserting coding for the domains into a
CC  phage expression vector; and (c) isolating the catalytic antibodies. The
CC  phage expression vector incorporates a histidine peptide in tandem with a
CC  myc peptide. The catalytic antibodies can be isolated by preparing an
CC  antigen, optionally immunising an animal with the antigen; generating a
CC  library of VH and VL domains from the immunised animal; cloning the VH
CC  and VL domains into a phage expression vector to generate phage display
CC  antibodies; selecting phage display antibodies which bind specifically to
CC  the antigen; screening the selected phage display antibodies for
CC  catalytic activity to substrate; and isolating the catalytic antibodies,
CC  where the phage expression vector incorporates a histidine peptide in
CC  tandem with a myc peptide. The processes are used to produce catalytic
CC  antibodies, which can be used for in vivo activation of a prodrg. The
CC  present sequence represents a genetic sequence of light chain pattern A
CC  from mouse derived RT3 phage antibodies
XX
SQ  Sequence 92 AA;
XX
Query Match      81.1%; Score 43; DB 2; Length 92;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY  1 RASODIGNSL 10
    |||||:|
DB  16 RASQDIGSSL 25
XX
Search completed: April 4, 2005, 15:47:15
Job time : 28.9649 secs

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## OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 16.2364 Seconds  
(without alignments)  
224.651 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_157\_167

Perfect score: 53

Sequence: 1 RASODIGSLRT 11

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
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8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
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16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	243	9	US-09-887-853-6
2	53	100.0	243	17	US-10-683-547-6
3	53	100.0	267	9	US-09-766-543-10
4	53	100.0	276	9	US-09-766-543-12
5	48	90.6	109	14	US-10-078-757B-55
6	45	84.9	112	14	US-10-355-780-1
7	43	81.1	108	14	US-10-010-729-45
8	43	81.1	108	16	US-10-803-622-267
9	43	81.1	108	16	US-10-803-653-267
10	43	81.1	109	9	US-09-943-906-74
11	43	81.1	109	15	US-10-435-602-74
12	43	81.1	130	8	US-08-779-784-35
13	43	81.1	130	14	US-10-010-729-71

14	43	81.1	144	16	US-10-642-120-4	Sequence 4, Appl1
15	43	81.1	144	16	US-10-642-060-4	Sequence 4, Appl1
16	43	81.1	144	16	US-10-642-122-4	Sequence 4, Appl1
17	43	81.1	144	16	US-10-642-124-4	Sequence 4, Appl1
18	43	81.1	144	16	US-10-621-269-4	Sequence 4, Appl1
19	43	81.1	144	16	US-10-620-850-4	Sequence 4, Appl1
20	43	81.1	144	16	US-10-642-100-4	Sequence 4, Appl1
21	43	81.1	144	17	US-10-642-100-4	Sequence 4, Appl1
22	43	81.1	144	17	US-10-642-058-4	Sequence 4, Appl1
23	43	81.1	144	17	US-10-642-121-4	Sequence 4, Appl1
24	43	81.1	154	15	US-10-239-656-55	Sequence 55, Appl1
25	43	81.1	257	15	US-10-239-656-57	Sequence 67, Appl1
26	43	81.1	499	15	US-10-239-656-73	Sequence 73, Appl1
27	42	79.2	11	10	US-09-155-106-4	Sequence 4, Appl1
28	42	79.2	11	17	US-10-808-538-4	Sequence 4, Appl1
29	42	79.2	108	10	US-09-155-106-22	Sequence 22, Appl1
30	42	79.2	108	10	US-09-155-106-23	Sequence 23, Appl1
31	42	79.2	108	10	US-09-155-106-24	Sequence 24, Appl1
32	42	79.2	108	10	US-09-155-106-28	Sequence 28, Appl1
33	42	79.2	108	10	US-09-155-106-30	Sequence 30, Appl1
34	42	79.2	108	17	US-10-808-538-22	Sequence 22, Appl1
35	42	79.2	108	17	US-10-808-538-23	Sequence 23, Appl1
36	42	79.2	108	17	US-10-808-538-24	Sequence 24, Appl1
37	42	79.2	108	17	US-10-808-538-28	Sequence 28, Appl1
38	42	79.2	108	17	US-10-808-538-30	Sequence 30, Appl1
39	42	79.2	109	14	US-10-078-757B-49	Sequence 49, Appl1
40	39	73.6	11	9	US-09-924-099-3	Sequence 3, Appl1
41	39	73.6	11	16	US-10-307-276B-38	Sequence 38, Appl1
42	39	73.6	12	15	US-10-411-869A-39	Sequence 39, Appl1
43	39	73.6	31	9	US-09-956-206A-3	Sequence 3, Appl1
44	39	73.6	95	9	US-09-943-906-72	Sequence 72, Appl1
45	39	73.6	95	15	US-10-435-602-72	Sequence 72, Appl1

## ALIGNMENTS

RESULT 1  
US-09-887-853-6  
Sequence 6, Application US/09887853  
Patent No. US20020168375A1  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
Oppermann, Hermann  
Houston, L. L.  
Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Teesta, Hurwitz & Thibault/Patent Department  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/887, 853  
FILING DATE: 21-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/133, 804  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-887-853-6

Query Match 100.0%; Score 53; DB 9; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11  
Db 157 RASODIGNSLT 167

RESULT 2  
US-10-683-547-6  
Sequence 6, Application US/10683547  
Publication No. US20050058638A1  
GENERAL INFORMATION:  
APPLICANT: Houston, J.  
APPLICANT: Ring, D.  
APPLICANT: Oppenmann, H.  
TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING  
FILE REFERENCE: CIBT-P01-130  
CURRENT APPLICATION NUMBER: US/10/683,547  
CURRENT FILING DATE: 2003-10-10  
PRIOR APPLICATION NUMBER: US/09/558,741  
PRIOR FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: 07/831,967  
PRIOR FILING DATE: 1992-02-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 6  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 520C9 sFv  
US-10-683-547-6

Query Match 100.0%; Score 53; DB 17; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11  
Db 157 RASODIGNSLT 167

RESULT 3  
US-09-766-543-10  
Sequence 10, Application US/09766543  
Patent No. US20020041865A1  
GENERAL INFORMATION:  
APPLICANT: Austin, Richard  
APPLICANT: Kwok, Cheuk S.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: METHODS FOR TREATING TUMORS  
FILE REFERENCE: PP01679.002  
CURRENT APPLICATION NUMBER: US/09/766,543  
CURRENT FILING DATE: 2000-01-19  
PRIOR APPLICATION NUMBER: 60/177,258  
PRIOR FILING DATE: 2000-01-20  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10

LENGTH: 267  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: 520C9  
OTHER INFORMATION: humanized single-chain antibody used in the  
OTHER INFORMATION: IL-2-antibody fusions  
US-09-766-543-10

Query Match 100.0%; Score 53; DB 9; Length 267;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11  
Db 176 RASODIGNSLT 186

RESULT 4  
US-09-766-543-12  
Sequence 12, Application US/09766543  
Patent No. US20020041865A1  
GENERAL INFORMATION:  
APPLICANT: Austin, Richard  
APPLICANT: Kwok, Cheuk S.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: METHODS FOR TREATING TUMORS  
FILE REFERENCE: PP01679.002  
CURRENT APPLICATION NUMBER: US/09/766,543  
CURRENT FILING DATE: 2000-01-19  
PRIOR APPLICATION NUMBER: 60/177,258  
PRIOR FILING DATE: 2000-01-20  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 276  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: H520C9sFv plus  
OTHER INFORMATION: linker  
US-09-766-543-12

Query Match 100.0%; Score 53; DB 9; Length 276;  
Best Local Similarity 100.0%; Pred. No. 0.052;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11  
Db 176 RASODIGNSLT 186

RESULT 5  
US-10-078-757B-55  
Sequence 55, Application US/10078757B  
Publication No. US20030166871A1  
GENERAL INFORMATION:  
APPLICANT: BARBAS, Carlos F., III  
APPLICANT: RADER, Christoph  
TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY  
FILE REFERENCE: TSRI 598.0 Con1  
CURRENT APPLICATION NUMBER: US/10/078,757B  
CURRENT FILING DATE: 2002-02-19  
PRIOR APPLICATION NUMBER: US 08/986,016  
PRIOR FILING DATE: 1997-12-05  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 55  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: hybrid mouse - human sequence

US-10-078-757B-55

Query Match 90.6%; Score 48; DB 14; Length 109;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASODIGNSL 10  
|||||:  
Db 24 RASODIGNSL 33

RESULT 6

US-10-355-780-1  
; Sequence 1, Application US/10355780  
; Publication No. US20030143224A1  
; GENERAL INFORMATION:  
; APPLICANT: Pusineri, Stanley  
; APPLICANT: Safar, Jiri  
; APPLICANT: Williamson, Anthony  
; APPLICANT: Burton, Dennis  
; TITLE OF INVENTION: Antibodies Specific for Ungulate PrP  
; FILE REFERENCE: UCAI-194  
; CURRENT APPLICATION NUMBER: US/10/355,780  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: US/09/627,2188  
; PRIOR FILING DATE: 2000-07-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 112  
; TYPE: PrP  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthesized peptide  
US-10-355-780-1

Query Match 84.9%; Score 45; DB 14; Length 112;  
Best Local Similarity 90.0%; Pred. No. 0.7;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASODIGNSL 10  
|||||:  
Db 24 RASODIGNSL 33

RESULT 7

US-10-010-729-45  
; Sequence 45, Application US/10010729  
; Publication No. US20030185827A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodriguez, Moses  
; APPLICANT: Miller, David J.  
; APPLICANT: Pease, Larry R.  
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and  
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous  
; TITLE OF INVENTION: System  
; FILE REFERENCE: 1199-1-005CIP2  
; CURRENT APPLICATION NUMBER: US/10/010,729  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: 09/730,473  
; PRIOR FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: 09/580,787  
; PRIOR FILING DATE: 2000-05-30  
; PRIOR APPLICATION NUMBER: 09/322,862  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 08/779,784  
; PRIOR FILING DATE: 1997-01-07  
; PRIOR APPLICATION NUMBER: 08/692,084  
; PRIOR FILING DATE: 1996-08-08  
; PRIOR APPLICATION NUMBER: 08/236,520  
; PRIOR FILING DATE: 1994-04-29  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 45  
; LENGTH: 108  
; TYPE: PrP  
; ORGANISM: Mus musculus  
US-10-010-729-45

Query Match 81.1%; Score 43; DB 14; Length 108;  
Best Local Similarity 90.0%; Pred. No. 1.7;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASODIGNSL 10  
|||||:  
Db 24 RASODIGNSL 33

RESULT 8

US-10-803-622-267  
; Sequence 267, Application US/10803622  
; Publication No. US20040157214A1  
; GENERAL INFORMATION:  
; APPLICANT: Cambridge Antibody Technology  
; APPLICANT: Cambridge Antibody Technology Limited  
; APPLICANT: Medical Research Council  
; APPLICANT: McCafferty, John  
; APPLICANT: Pope, Anthony  
; APPLICANT: Johnson, Kevin  
; APPLICANT: Hoogendoorn, Hendricus  
; APPLICANT: Griffiths, Andrew  
; APPLICANT: Jackson, Ronald  
; APPLICANT: Holliger, Kasper  
; APPLICANT: Marks, James  
; APPLICANT: Jackson, Timothy  
; APPLICANT: Chiswell, David  
; APPLICANT: Winter, Gregory  
; APPLICANT: Bonert, Timothy  
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
; FILE REFERENCE: 13839-00013  
; CURRENT APPLICATION NUMBER: US/10/803,622  
; CURRENT FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: GB 9015198.6  
; PRIOR FILING DATE: 1990-07-10  
; PRIOR APPLICATION NUMBER: GB 9022845.3  
; PRIOR FILING DATE: 1990-10-19  
; PRIOR APPLICATION NUMBER: GB 9022845.3  
; PRIOR FILING DATE: 1990-10-19  
; PRIOR APPLICATION NUMBER: GB 9022845.3  
; PRIOR FILING DATE: 1990-10-19  
; PRIOR APPLICATION NUMBER: GB 9024503.6  
; PRIOR FILING DATE: 1990-11-12  
; PRIOR APPLICATION NUMBER: GB 9104744.9  
; PRIOR FILING DATE: 1991-03-06  
; PRIOR APPLICATION NUMBER: GB 9110549.4  
; PRIOR FILING DATE: 1991-05-15  
; PRIOR APPLICATION NUMBER: PCT/GB91/01134  
; PRIOR FILING DATE: 1991-07-10  
; PRIOR APPLICATION NUMBER: US 07/971,857  
; PRIOR FILING DATE: 1993-01-08  
; PRIOR APPLICATION NUMBER: US 08/484,893  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 272  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 267  
; LENGTH: 108  
; TYPE: PrP  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: light chain from clone M1F  
US-10-803-622-267

Query Match 81.1%; Score 43; DB 16; Length 108;  
Best Local Similarity 90.0%; Pred. No. 1.7;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASODIGNSL 10  
|||||:  
Db 24 RASODIGNSL 33

Db 24 RASODIGSSL 33

RESULT 9

US-10-803-653-267

Sequence 267, Application US/10803653

Publication No. US20040157215A1

GENERAL INFORMATION:

APPLICANT: Cambridge Antibody Technology

APPLICANT: Cambridge Antibody Technology Limited

APPLICANT: Medical Research Council

APPLICANT: McCafferty, John

APPLICANT: Pope, Anthony

APPLICANT: Johnson, Kevin

APPLICANT: Hoogenboom, Hendricus

APPLICANT: Griffiths, Andrew

APPLICANT: Jackson, Ronald

APPLICANT: Holliger, Kasper

APPLICANT: Marks, James

APPLICANT: Clackson, Timothy

APPLICANT: Chiswell, David

APPLICANT: Winter, Gregory

APPLICANT: Bonert, Timothy

TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs

FILE REFERENCE: 13839-00013

CURRENT APPLICATION NUMBER: US/10/803,653

CURRENT FILING DATE: 2004-03-18

PRIOR APPLICATION NUMBER: GB 9015198.6

PRIOR FILING DATE: 1990-07-10

PRIOR APPLICATION NUMBER: GB 9022845.3

PRIOR FILING DATE: 1990-10-19

PRIOR APPLICATION NUMBER: GB 9022845.3

PRIOR FILING DATE: 1990-10-19

PRIOR APPLICATION NUMBER: GB 9024503.6

PRIOR FILING DATE: 1990-11-12

PRIOR APPLICATION NUMBER: GB 9104744.9

PRIOR FILING DATE: 1991-03-06

PRIOR APPLICATION NUMBER: GB 9110549.4

PRIOR FILING DATE: 1991-05-15

PRIOR APPLICATION NUMBER: PCT/GB91/01134

PRIOR FILING DATE: 1991-07-10

PRIOR APPLICATION NUMBER: US 07/971,857

PRIOR FILING DATE: 1993-01-08

PRIOR APPLICATION NUMBER: US 08/484,893

PRIOR FILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 272

SOFTWARE: PatentIn version 3.1

SEQ ID NO 267

LENGTH: 108

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: light chain from clone M1F

US-10-803-653-267

Query Match 81.1%; Score 43; DB 16; Length 108;

Best Local Similarity 90.0%; Pred. No. 1.7;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGSSL 10

Db 24 RASODIGSSL 33

RESULT 10

US-09-943-906-74

Sequence 74, Application US/09943906

Patent No. US20020150571A1

GENERAL INFORMATION:

APPLICANT: Prusiner, Stanley B.

APPLICANT: Williamson, R. Anthony

APPLICANT: Burton, Dennis R.

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 2200 Sand Hill Road

CITY: Menlo Park

STATE: CA

COUNTRY: U.S.A.

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/943,906

FILING DATE: 30-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/550,374

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Bozicevic, Karl

REGISTRATION NUMBER: 28,807

REFERENCE/DOCKET NUMBER: 06510/059001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-5277

TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 74:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 74:

US-09-943-906-74

Query Match 81.1%; Score 43; DB 9; Length 109;

Best Local Similarity 90.0%; Pred. No. 1.7;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGSSL 10

Db 24 RASODIGSSL 33

RESULT 11

US-10-435-602-74

Sequence 74, Application US/10435602

Publication No. US20030228303A1

GENERAL INFORMATION:

APPLICANT: Prusiner, Stanley B.

APPLICANT: Williamson, R. Anthony

APPLICANT: Burton, Dennis R.

TITLE OF INVENTION: Antibodies Specific for Native PrPsc

FILE REFERENCE: UCAL059CON3

CURRENT APPLICATION NUMBER: US/10/435,602

CURRENT FILING DATE: 2003-05-09

PRIOR APPLICATION NUMBER: 09/943,906

PRIOR FILING DATE: 2001-08-30

PRIOR APPLICATION NUMBER: 09/550,374

PRIOR FILING DATE: 2000-04-13

PRIOR APPLICATION NUMBER: 09/036,579

PRIOR FILING DATE: 1998-03-06

PRIOR APPLICATION NUMBER: 08/713,939

PRIOR FILING DATE: 1996-09-13

PRIOR APPLICATION NUMBER: 08/528,104

PRIOR FILING DATE: 1995-09-14

NUMBER OF SEQ ID NOS: 86

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 74

LENGTH: 109

TYPE: PRT  
ORGANISM: mouse  
US-10-435-602-74

Query Match 81.1%; Score 43; DB 15; Length 109;  
Best Local Similarity 90.0%; Pred. No. 1.7;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSL 10  
DB 24 RASODIGSSL 33

## RESULT 12

US-08-779-784-35  
Sequence 35, Application US/08779784  
Publication No. US20020164325A1  
GENERAL INFORMATION:  
APPLICANT: Rodriguez, Moses  
APPLICANT: Miller, David J.  
APPLICANT: Asakura, Kunihiko  
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESS: David A. Jackson, Esq.,  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
FLOOR  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/779,784  
FILING DATE: 07-JAN-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/692,084  
FILING DATE: 08-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/236,520  
FILING DATE: 29-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus  
US-08-779-784-35

Query Match 81.1%; Score 43; DB 8; Length 130;  
Best Local Similarity 90.0%; Pred. No. 2;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RASODIGNSL 10  
DB 11 RASODIGSSL 10

DB 46 RASODIGSSL 55

## RESULT 13

US-10-010-729-71  
Sequence 71, Application US/10010729  
Publication No. US20030185827A1  
GENERAL INFORMATION:  
APPLICANT: Rodriguez, Moses  
APPLICANT: Miller, David J.  
APPLICANT: Pease, Larry R.  
TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and  
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous  
SYSTEM  
FILE REFERENCE: 1199-1-005C1P2  
CURRENT APPLICATION NUMBER: US/10/010,729  
CURRENT FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: 09/730,473  
PRIOR FILING DATE: 2000-12-05  
PRIOR APPLICATION NUMBER: 09/580,787  
PRIOR FILING DATE: 2000-05-30  
PRIOR APPLICATION NUMBER: 09/322,862  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 08/779,784  
PRIOR FILING DATE: 1997-01-07  
PRIOR APPLICATION NUMBER: 08/692,084  
PRIOR FILING DATE: 1996-08-08  
PRIOR APPLICATION NUMBER: 08/236,520  
PRIOR FILING DATE: 1994-04-29  
NUMBER OF SEQ ID NOS: 80  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 71  
LENGTH: 130  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-010-729-71

Query Match 81.1%; Score 43; DB 14; Length 130;  
Best Local Similarity 90.0%; Pred. No. 2;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSL 10  
DB 46 RASODIGSSL 55

## RESULT 14

US-10-642-120-4  
Sequence 4, Application US/10642120  
Publication No. US20040131610A1  
GENERAL INFORMATION:  
APPLICANT: Thorpe, Philip E.  
APPLICANT: Soares, M. Melina  
APPLICANT: Ran, Sophia  
TITLE OF INVENTION: Methods for Treating Viral Infections Using Antibodies to  
FILE REFERENCE: 4001.002900  
CURRENT APPLICATION NUMBER: US/10/642,120  
CURRENT FILING DATE: 2003-08-15  
PRIOR APPLICATION NUMBER: US 10/621,269  
PRIOR FILING DATE: 2003-07-15  
PRIOR APPLICATION NUMBER: 60/396,263  
PRIOR FILING DATE: 2002-07-15  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 144  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-642-120-4

Query Match 81.1%; Score 43; DB 16; Length 144;  
Best Local Similarity 90.0%; Pred. No. 2.3;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
|||:|  
Db 46 RASQDIGSSL 55

RESULT 15

US-10-642-060-4  
; Sequence 4, Application US/10642060  
; Publication No. US20040131621A1  
; GENERAL INFORMATION:  
; APPLICANT: Thorpe, Philip E.  
; APPLICANT: Soares, M. Melina  
; APPLICANT: Ran, Sophia  
; TITLE OF INVENTION: Combinations and Kits for Treating Viral Infections Using Antibod  
; FILE REFERENCE: 4001.002982  
; CURRENT APPLICATION NUMBER: US/10/642,060  
; CURRENT FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: US 10/621,269  
; PRIOR FILING DATE: 2003-07-15  
; PRIOR APPLICATION NUMBER: 60/396,263  
; PRIOR FILING DATE: 2002-07-15  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-642-060-4

Query Match 81.1%; Score 43; DB 16; Length 144;  
Best Local Similarity 90.0%; Pred. No. 2.3;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
|||:|  
Db 46 RASQDIGSSL 55

Search completed: April 4, 2005, 16:42:44  
Job time : 16.2364 secs



GenCore version 5.1.6  
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OM protein - protein search, using ew model

Run on: April 4, 2005, 15:32:36 ; Search time 3.97125 seconds  
(without alignments)  
266.512 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_157\_167

Perfect score: 53

Sequence: 1 RASODIGNSLT 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	81.1	88	2	PI0261
2	43	81.1	106	2	PI0260
3	43	81.1	130	1	KVMSM4
4	42	79.2	106	2	PI0259
5	41	77.4	108	2	S40330
6	39	73.6	95	2	PH0865
7	38	71.7	91	2	S37511
8	38	71.7	281	2	S54137
9	37	69.8	108	2	S19970
10	37	69.8	114	2	S00996
11	37	69.8	125	2	S40353
12	37	69.8	127	2	PH1224
13	37	69.8	312	2	B96512
14	36	67.9	53	2	PH0881
15	36	67.9	93	2	S38564
16	36	67.9	107	2	S69901
17	36	67.9	107	2	S32188
18	36	67.9	107	2	A28044
19	36	67.9	107	2	D48677
20	36	67.9	107	2	B28044
21	36	67.9	107	2	B49026
22	36	67.9	107	2	S69901
23	36	67.9	108	1	KIHUBI
24	36	67.9	108	1	KVMSAR
25	36	67.9	108	2	PI0282
26	36	67.9	108	2	C30502
27	36	67.9	108	2	B30551
28	36	67.9	108	2	C26405
29	36	67.9	108	2	B26405

30	36	67.9	108	2	S38862	Ig kappa chain V r
31	36	67.9	108	2	S69902	Ig kappa chain (cl
32	36	67.9	108	2	S69900	Ig kappa chain (cl
33	36	67.9	108	2	S69903	Ig kappa chain (cl
34	36	67.9	115	2	A53276	Ig kappa chain V r
35	36	67.9	115	2	JI0080	Ig kappa chain pre
36	36	67.9	122	2	A29380	Ig kappa chain pre
37	36	67.9	126	2	A34904	Ig kappa chain pre
38	36	67.9	128	2	A28406	Ig kappa chain V r
39	36	67.9	298	2	B75429	hypothetical prote
40	36	67.9	730	2	B83592	hypothetical prote
41	35	66.0	125	2	S04936	Ig kappa chain pre
42	35	66.0	130	2	PI0113	Ig kappa chain pre
43	35	66.0	139	2	S40365	Ig kappa chain h
44	35	66.0	422	1	KKHUZ	plasma protein 2 p
45	34	64.2	87	2	PH1082	Ig light chain V r

#### ALIGNMENTS

```
RESULT 1
PI0261
Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997
C/Accession: PI0261
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pletscky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A/Reference number: PI0231; MUID:90111618; PMID:2104919
A/Accession: PI0261
A/Molecule type: mRNA
A/Residues: 1-88 <SHL>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F.1-5/Region: framework 1
F.6-16/Region: complementarity-determining 1
F.17-31/Region: framework 2
F.32-38/Region: complementarity-determining 2
F.39-70/Region: framework 3
F.71-79/Region: complementarity-determining 3
F.80-88/Region: framework 4

Query Match      81.1%; Score 43; DB 2; Length 88;
Best Local Similarity 90.0%; Pred. No. 0.2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASODIGNSLT 10
DB      6 RASODIGSL 15

RESULT 2
PI0260
Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pletscky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A/Reference number: PI0231; MUID:90111618; PMID:2104919
A/Accession: PI0260
A/Molecule type: mRNA
A/Residues: 1-106 <SHL>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F.1-23/Region: framework 1
F.16-30/Domain: immunoglobulin homology <IMW>
F.24-34/Region: complementarity-determining 1
F.35-49/Region: framework 2
F.50-56/Region: complementarity-determining 2
```

F:57-88/Region: framework 3  
F:89-97/Region: complementarity-determining 3  
F:98-106/Region: framework 4

Query Match 81.1%; Score 43; DB 2; Length 106;  
Best Local Similarity 90.0%; Pred. No. 0.24;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
DB 24 RASQDIGSSL 33

## RESULT 3

KVMSM4  
Ig kappa chain precursor V region (MOPC 41) - mouse  
N/Contexts: Ig kappa chain precursor V region VK41  
C/Species: Mus musculus (house mouse)  
C/Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text change 09-Jul-2004  
C/Accession: A93211; B93211; A93815; A94239; A01922; A01523  
R/Seidman, J.G.; Max, E.R.; Leder, P.  
Nature 280, 370-375, 1979

A/Title: A kappa-immunoglobulin gene is formed by site-specific recombination without fu  
A/Reference number: A93211; MUID:79221900; PMID:111146

A/Accession: A93211

A/Molecule type: DNA

A/Residues: 1-130 <PC41>

A/Cross-references: UNIPROT:P01639

A/Accession: B93211

A/Molecule type: DNA

A/Residues: 1-117 <VK41>

A/Cross-references: GB:V00804; GB:J00566; NID:952127; PIDN:CA24186.1; PID:9575660

A/Note: the sequences were determined from the differentiated gene MOPC 41 and the germi

R/Burstein, Y.; Schacher, I.

Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977

A/Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursor

A/Reference number: A93815; MUID:77148916; PMID:403522

A/Accession: A93815

A/Molecule type: protein

A/Residues: 1-33 <BUR>

A/Note: Met-3 is apparently used as an alternative initiator in 25% of the chains

R/Gray, W.R.; Dreyer, W.J.; Hood, L.

Science 155, 465-467, 1967

A/Title: Mechanism of antibody synthesis: size differences between mouse kappa chains.

A/Reference number: A94239; MUID:67056897; PMID:4162331

A/Accession: A94239

A/Molecule type: protein

A/Residues: 23-49; B',51-53,'USB',57-58,'ZZ',61-62,'BZ',65-76,'B',78-108,110-130 <GRA>

A/Experimental source: Bence Jones protein MOPC 41

C/Genetics:

A/Introns: 19/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: alternative initiators; heterotetramer; immunoglobulin

F:1-22/Domain: signal sequence #status experimental <SIG1>

F:23-22/Domain: signal sequence #status experimental <SIG2>

F:23-130/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>

F:38-112/Domain: immunoglobulin homology <IMM>

F:45-110/Disulfide bonds: #status predicted

Query Match 81.1%; Score 43; DB 1; Length 130;  
Best Local Similarity 90.0%; Pred. No. 0.3;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
DB 46 RASQDIGSSL 55

## RESULT 4

PL0259  
Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 16-Sep-1992 #sequence revision 16-Sep-1992 #text change 21-Jan-2000

C/Accession: PL0259

R/Shlomchik, M.; Maccelli, M.; Shan, H.; Radic, M.Z.; Pisetky, D.; Marshak-Rohstein, A

J. Exp. Med. 171, 265-297, 1990

A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n

A/Reference number: PL0231; MUID:90111618; PMID:2104919

A/Accession: PL0259

A/Molecule type: mRNA

A/Residues: 1-106 <SHL>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3

F:89-97/Region: complementarity-determining 3

F:98-106/Region: framework 4

Query Match 79.2%; Score 42; DB 2; Length 106;  
Best Local Similarity 90.0%; Pred. No. 0.38;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
DB 24 RASQDIGSSL 33

## RESULT 5

S40330  
Ig kappa chain V-J region - human

C/Species: Homo sapiens (man)

C/Date: 19-May-1994 #sequence revision 26-May-1995 #text change 23-Jul-1999

C/Accession: S40330

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40330

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-108 <KLE>

A/Cross-references: EMBL:X72440; NID:9441348; PIDN:CA51108.1; PID:9441349

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 77.4%; Score 41; DB 2; Length 108;  
Best Local Similarity 90.0%; Pred. No. 0.62;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
DB 27 RASQDIGSSL 36

## RESULT 6

PH0865  
Ig kappa chain V region (anti-DNA, I-2a) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 09-Oct-1992 #sequence revision 09-Oct-1992 #text change 21-Jan-2000

C/Accession: PH0865

R/Manheiser-Loty, A.; Katz, J.B.; Pillinger, M.; Ghosein, C.; Smith, A.; Diamond, B.

J. Exp. Med. 174, 1639-1652, 1991

A/Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.

A/Reference number: PH0862; MUID:92078875; PMID:1660528

A/Accession: PH0865

A/Molecule type: DNA

A/Residues: 1-95 <MAN>

C/Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

```

F.15-23/Region: framework 1
F.16-90/Domain: immunoglobulin homology <IMM>
F.24-34/Region: complementarity-determining 1
F.35-49/Region: framework 2
F.50-56/Region: complementarity-determining 2
F.57-88/Region: framework 3
F.89-95/Region: complementarity-determining 3

Query Match
Best Local Similarity 73.6%; Score 39; DB 2; Length 95;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11
   |||||
Db 24 RASODIRNYLT 34

RESULT 7
S37511
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37511
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37511
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <KLE>
A:Cross-references: EMBL,Z26600; NID:G405664; PIDN:CAA61354.1; PID:G405665
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin

Query Match
Best Local Similarity 71.7%; Score 38; DB 2; Length 91;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 10
   ||||
Db 7 RASQSVGNLT 16

RESULT 8
S54137
probable movement protein - asparagus virus II
C:Species: asparagus virus II
C>Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: S54137
R:Rafaeli-Martin, M.; Rivera-Bustamante, R.F.
submitted to the EMBL Data Library, April 1995
A:Description: Nucleotide sequence of asparagus virus II (AVIR) RNA3.
A:Reference number: S54137
A:Accession: S54137
A:Molecule type: genomic RNA
A:Residues: 1-281 <ROM>
A:Cross-references: UNIPROT:Q65298; EMBL:X86352; NID:G807865; PIDN:CAA60124.1; PID:G8083
A:Experimental source: isolate Mexican
C:Superfamily: alfalfa mosaic virus 32.4K protein

Query Match
Best Local Similarity 71.7%; Score 38; DB 2; Length 281;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11
   |||||
Db 176 RYSEDVGSSTLT 186

RESULT 9
S19970
Ig kappa chain V region (M-T151) - mouse (fragment)

```

```

C:Species: Mus musculus (house mouse)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S19970
R:Weissenhorn, W., Riethmueler, G., Weiss, E.M., Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mab.
A/Reference number: S19963
A/Accession: S19970
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <WEB>
A/Cross-references: EMBL:X65095; NID:952286; PIDN:CAA46223.1; PID:955287
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match          69.8%; Score 37; DB 2; Length 108;
Best Local Similarity 72.7%; Pred. No. 4;
Matches      8; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

QY      1 RASQDIGNSLT 11
        |||||
        24 RASQDINNYLS 34

RESULT 10
S00996
IG kappa chain precursor V region (A10) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jul-1999
C/Accession: S00996
R:Strandinger, B., Thiele, R., Huber, C., Osterholzer, E., Zachau, H.G.
Bio1. Chem. Hoppe-Seyler 369, 601-607, 1988
A/Title: Two unusual human immunoglobulin V-kappa genes.
A/Reference number: S00996; MUID:89134397; PMID:2852016
A/Accession: S00996
A/Molecule type: DNA
A/Residues: 1-114 <STR>
A/Cross-references: EMBL:M27750; NID:9185914; PIDN:AAA58912.1; PID:9553479
A/Note: this sequence was determined from the germline gene
C/Genetics:
A/Ions: 16/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-11/Product: Ig kappa chain V region #status predicted <MAT>
F:42-107/Disuulfide bonds: #status predicted

Query Match          69.8%; Score 37; DB 2; Length 114;
Best Local Similarity 80.0%; Pred. No. 4.2;
Matches      8; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

QY      1 RASQDIGNSL 10
        |||||
        43 RASQIGSSSL 52

RESULT 11
S40353
IG kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40353
R:Klein, R., Jaenichen, R., Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40353
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-125 <KBL>
A/Cross-references: EMBL:X72463
C/Superfamily: immunoglobulin V region; immunoglobulin homology

```

C:Keywords: heterotetramer; immunoglobulin  
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 37; DB 2; Length 125;  
Best Local Similarity 80.0%; Pred. No. 4.7;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
DB 38 RASQDIGNSL 47

## RESULT 12

PH1224  
Ig kappa chain precursor V region (M-T151) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 21-Jan-2000

C:Accession: PH1224

R:Weissenborn, W.; Scheuer, W.; Kaluza, B.; Schwitzke, M.; Reiter, C.; Flieger, D.; Lenz  
Gene 121, 271-278, 1992

A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on  
F:36-110/Domain: immunoglobulin homology <IMM>

A:Reference number: PH1224; PMID:93077041; PMID:1446824

A:Accession: PH1224

A:Molecule type: mRNA  
A:Residues: 1-127 <WEI>

A:Cross-references: GB:S50261; NID:g260761; PIDN:AA24318.1; PID:g260762  
A:Note: this mouse sequence was hybridized and fused with a human constant region gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-127/Product: Ig light chain V region #status predicted <MAT>

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 37; DB 2; Length 127;  
Best Local Similarity 72.7%; Pred. No. 4.7;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 11  
DB 44 RASQDIGNSL 54

## RESULT 13

B96512  
hypothetical protein F2G19.20 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: B96512  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
aneen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marshall,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; PMID:21016719; PMID:11130712

A:Accession: B96512

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-312 <STO>

A:Cross-references: UNIPROT:Q9C628; GB:AE005173; NID:g11321767; PIDN:AA34244.1; GSPDB:C  
C:Genetics:

A:Gene: F2G19.20

A:Map position: 1

Query Match 69.8%; Score 37; DB 2; Length 312;  
Best Local Similarity 70.0%; Pred. No. 12;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
DB 1 RASQDIGNSL 10

DB 289 KVSQDIGNSL 298

## RESULT 14

PH0881  
Ig kappa chain V region (GOU) - human (fragment)

N:Alternate names: myeloma protein  
C:Species: Homo sapiens (man)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 09-May-1997

C:Accession: PH0881

R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghosein, C.; Smith, A.; Diamond, B.  
J. Exp. Med. 174, 1639-1652, 1991

A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.  
A:Reference number: PH0882; PMID:92078875; PMID:160528

A:Accession: PH0881

A:Molecule type: protein  
A:Residues: 1-53 <MAN>

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1  
F:24-34/Region: complementarity-determining 1  
F:35-49/Region: framework 2  
F:50-53/Region: complementarity-determining 2

Query Match 67.9%; Score 36; DB 2; Length 53;  
Best Local Similarity 80.0%; Pred. No. 3;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
DB 24 RASQDIGNSL 33

## RESULT 15

S38564  
Ig kappa chain V region (ASWU) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C:Accession: S38564

R:Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.  
submitted to the EMBL Data Library, September 1993

A:Description: Molecular analysis of mercury-induced anti-nuclear antibodies in H-2s M  
A:Reference number: S38559

A:Accession: S38564

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-93 <MON>

A:Cross-references: EMBL:X75105; NID:g414153; PIDN:CAA52996.1; PID:g414154  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 67.9%; Score 36; DB 2; Length 93;  
Best Local Similarity 80.0%; Pred. No. 5.5;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
DB 24 RASQDIGNSL 33

Search completed: April 4, 2005, 15:58:01  
Job time : 4.97125 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 18.5911 seconds  
(without alignments)  
302.988 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_157\_167  
Perfect score: 53  
Sequence: 1 RASQDIGNSLT 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	81.1	130	1	KV5G_MOUSE
2	40	75.5	365	2	Q65SM6
3	38	71.7	281	2	Q65298
4	38	71.7	283	2	Q98702
5	38	71.7	283	2	Q91MN5
6	37	69.8	312	2	Q9C628
7	37	69.8	447	2	Q6R6C8
8	37	69.8	4091	2	Q7QNA8
9	36	67.9	108	1	KVIC_HUMAN
10	36	67.9	108	1	KV5K_MOUSE
11	36	67.9	108	1	KV5L_MOUSE
12	36	67.9	108	1	KV5M_MOUSE
13	36	67.9	108	1	KV5N_MOUSE
14	36	67.9	108	1	KV5O_MOUSE
15	36	67.9	127	2	Q925S9
16	36	67.9	133	2	Q6CRP8
17	36	67.9	236	2	Q7Z3Y4
18	36	67.9	288	1	Q6MMU3
19	36	67.9	298	1	UB72_DEIRA
20	36	67.9	423	2	Q6R6T3
21	36	67.9	515	2	Q9FVDS
22	36	67.9	730	2	Q91683
23	36	67.9	1222	2	Q87XX8
24	35	66.0	133	2	Q9QOV6
25	35	66.0	166	2	Q7WZP4
26	35	66.0	236	2	Q6GFP1
27	35	66.0	282	2	Q57164
28	35	66.0	283	2	O11876
29	35	66.0	339	2	Q7MDB0
30	35	66.0	342	1	MURB_RALSO
31	35	66.0	348	2	Q8D6F5

32	35	66.0	349	2	Q87IS9	Q87IS9 vibrio para
33	35	66.0	374	2	O05107	O05107 ectothiorho
34	35	66.0	400	1	PRTZ_HUMAN	P22891 homo sapien
35	35	66.0	490	2	Q8PDC1	Q8PDC1 xanthomonas
36	35	66.0	535	2	Q822S9	Q822S9 chlamydomon
37	35	66.0	867	2	Q8XCF2	Q8XCF2 neurospora
38	35	66.0	1134	2	Q7YVE0	Q7YVE0 cryptospori
39	35	66.0	1338	2	Q75JG1	Q75JG1 dictyostell
40	34	64.2	81	2	Q9NPB5	Q9NPB5 homo sapien
41	34	64.2	108	1	KVIG_HUMAN	Q9NPB5 homo sapien
42	34	64.2	108	1	P01599	P01599 homo sapien
43	34	64.2	115	1	KVSI_MOUSE	P01642 mus musculu
44	34	64.2	199	2	Q65VU1	Q65VU1 manheimia
45	34	64.2	257	2	Q62HW0	Q62HW0 burkholderi

## ALIGNMENTS

RESULT 1	KV5G_MOUSE	STANDARD;	PRT;	130 AA.
ID	P01639; P01640;			
AC	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Ig kappa chain V-V region MOPC 41 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=79221900; PubMed=111146;			
RA	Seidman J.G., Max E.E., Leder P.;			
RT	"A kappa-immunoglobulin gene is formed by site-specific recombination			
RT	without further somatic mutation.";			
RL	Nature 280:370-375 (1979).			
RN	[2]			
RP	SEQUENCE OF 1-33.			
RX	MEDLINE=77148916; PubMed=403522;			
RA	Buretein Y., Schechter I.;			
RT	"Amino acid sequence of the NH2-terminal extra piece segments of the			
RT	precursors of mouse immunoglobulin lambda1-c type and kappa-type light			
RL	chains.";			
RN	Proc. Natl. Acad. Sci. U.S.A. 74:716-720 (1977).			
RN	[3]			
RP	SEQUENCE OF 23-130.			
RX	MEDLINE=67056897; PubMed=4162911;			
RA	Gray W.R., Dreyer W.U., Hood L.;			
RT	"Mechanism of antibody synthesis: size differences between mouse kappa			
RT	chains.";			
RL	Science 155:465-467 (1967).			
CC	- I- MICCELIANOUS; This precursor was synthesized in a cell-free			
CC	system directed by mRNA isolated from myeloma polyosomes.			
CC	- I- MICCELIANOUS; This is a Bence-Jones protein.			
CC	- I- MICCELIANOUS; This is a Bence-Jones protein.			
DR	PIR; A93211; KVM5M4.			
DR	HSSP; P01594; 1JVS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IgV_1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Bence-Jones protein; Direct protein sequencing;			
FT	Immunoglobulin V region; Signal.			
FT	SIGNAL	1	22	
FT	CHAIN	23	130	Ig kappa chain V-V region MOPC 41.
FT	DOMAIN	23	45	Framework-1.
FT	DOMAIN	46	56	Complementarity-determining-1.
FT	DOMAIN	57	71	Framework-2.
FT	DOMAIN	72	78	Complementarity-determining-2.
FT	DOMAIN	79	110	Framework-3.
FT	DOMAIN	111	119	Complementarity-determining-3.

FT DOMAIN 120 129 Framework-4.  
FT DISUPID 45 110 By similarity.  
FT VARIANT 1 2 Missing (in 25% of the molecules).  
FT NON\_TER 130 130  
SQ SEQUENCE 130 AA; 14311 MW; 5E9E0FE71D5F1BEC CRC64;

Query Match 81.1%; Score 43; DB 1; Length 130;  
Best Local Similarity 90.0%; Pred. No. 1.5;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASODIGNSLT 10  
Db 46 RASODIGSSL 55

RESULT 2  
ID O65SW6 PRELIMINARY; PRT; 365 AA.  
AC O65SW6;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE OmpC protein.  
GN Name=ompC; ORFNames=M51337;  
OS Mannheimia succiniciproducens MBE155.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Mannheimia.  
OX NCBI\_TaxID=221988;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MBE155;  
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,  
RA Kim C.H., Jeong H., Hur C.-G., Kim J.G.,  
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia  
succiniciproducens.";  
RL Nat. Biotechnol. 0:0-0(2004).  
EMBL; AE016827; AAU37944.1; -.  
SQ SEQUENCE 365 AA; 40255 MW; 83DD67AF0F30BF27 CRC64;

Query Match 75.5%; Score 40; DB 2; Length 365;  
Best Local Similarity 63.6%; Pred. No. 19;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASODIGNSLT 11  
Db 65 KASODIGNLS 75

RESULT 3  
ID O65298 PRELIMINARY; PRT; 281 AA.  
AC O65298;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Putative movement protein.  
GN Name=ORP1;  
OS Asparagus virus 2.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;  
OC Ilarvirus.  
OX NCBI\_TaxID=39681;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rafael-Martin M., Rivera-Bustamante R.F.,  
RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X86352; CAA60124.1; -.  
DR PIR; S54137; S54137.  
DR InterPro; IPR002538; Bromo\_MP.  
DR Pfam; PF01573; Bromo\_MP; 1.  
SQ SEQUENCE 281 AA; 31476 MW; 891B345872FC2E25 CRC64;

Query Match 71.7%; Score 38; DB 2; Length 281;  
Best Local Similarity 63.6%; Pred. No. 36;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 RASODIGNSLT 11  
Db 176 RYSEDVGSST 186

RESULT 4  
ID Q98702 PRELIMINARY; PRT; 283 AA.  
AC Q98702;  
DT 01-FEB-1997 (TReMBLrel. 02, Created)  
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Movement protein.  
OS Elm mottle virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;  
OC Ilarvirus.  
OX NCBI\_TaxID=56486;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97372954; PubMed=9229009;  
RA Ge X., Scott S.W., Zimmerman M.T.,  
RT "The complete sequence of the genomic RNAs of spinach latent virus.";  
RL Arch. Virol. 142:1213-1226(1997).  
DR EMBL; U57048; AA897770.1; -.  
DR InterPro; IPR002538; Bromo\_MP.  
DR Pfam; PF01573; Bromo\_MP; 1.  
SQ SEQUENCE 283 AA; 31508 MW; 9D3B923A8748BB6A CRC64;

Query Match 71.7%; Score 38; DB 2; Length 283;  
Best Local Similarity 63.6%; Pred. No. 36;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASODIGNSLT 11  
Db 176 RYSEDVGSST 186

RESULT 5  
ID Q91MN5 PRELIMINARY; PRT; 283 AA.  
AC Q91MN5;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE Putative movement protein 3a.  
OS Hydrangea mosaic virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;  
OC Ilarvirus.  
OX NCBI\_TaxID=42812;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22897981; PubMed=14551826;  
RA Scott S.W., Zimmerman M.T., Ge X.,  
RT "Viruses in subgroup 2 of the genus Ilarvirus share both serological  
relationships and characteristics at the molecular level.";  
RL Arch. Virol. 148:2063-2075(2003).  
DR EMBL; AF172965; AAF89807.1; -.  
DR InterPro; IPR002538; Bromo\_MP.  
DR Pfam; PF01573; Bromo\_MP; 1.  
SQ SEQUENCE 283 AA; 31508 MW; 863CD623774291A5 CRC64;

Query Match 71.7%; Score 38; DB 2; Length 283;  
Best Local Similarity 63.6%; Pred. No. 36;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASODIGNSLT 11  
Db 176 RYSEDVGSST 186

RESULT 6

```
09C628      PRELIMINARY;      PRT;      312 AA.
ID 09C628;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein F2G19.20.
GN Name=F2G19.20;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Rongling C.M., Xoo H., Fujii C.Y., Utecherack T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC083835; AAC50622.1; -.
DR PIR; B96512; B96512.
DR InterPro; IPR006527; F_box_assoc.1.
DR TIGRFAMs; TIGR01640; F_box_assoc_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 312 AA; 36256 MW; 025F1B0740B8F940 CRC64;

Query Match      69.8%; Score 37; DB 2; Length 312;
Best Local Similarity 70.0%; Pred. No. 64;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 RASODIGNSLT 10
Db 289 KVSRDIGNSLT 298

RESULT 7
06R6C8      PRELIMINARY;      PRT;      847 AA.
ID 06R6C8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE AcetA.
GN Name=acetA;
OS Listeria ivanovi subsp. londoniensis.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OC NCBI_TaxID=202752;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NRL 33021;
RA Ward T.J., Gorski L., Bornucki M.K., Mandrell R.E., Hutchins J.,
RA Pupedis K.;
RT "Interspecific Phylogeny and Lineage Group Identification Based on the
RT prfA Virulence Gene Cluster of Listeria monocytogenes.";
RL J. Bacteriol. 186:4994-5002(2004).
DR EMBL; AY510073; AAR97354.1; -.
DR InterPro; IPR007752; AcetA.
DR Pfam; PF05058; AcetA; 1.
SQ SEQUENCE 847 AA; 92364 MW; D9B407E0F8A5A13 CRC64;

Query Match      69.8%; Score 37; DB 2; Length 847;
Best Local Similarity 45.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
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DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE AGCP14079 (Fragment).
GN Name=agCG48186; ORFNames=ENSANG00000014545;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OC NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=PEST;
RC Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008898; EAA09222.1; -.
DR HSRP; Q01082; IBKR.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR001449; PH.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR001605; Spectrin_PH.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00307; CH; 2.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00019; SH3_1; 1.
DR Pfam; PF00435; Spectrin_31.
DR PRINTS; PR00683; SPECTRINPH.
DR ProDom; PD000066; SH3; 1.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS00021; CH; 2.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00002; SH3; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KW SH3 domain.
FT NON_TER 1
FT NON_TER 4091
FT NON_TER 4091
SQ SEQUENCE 4091 AA; 469663 MW; B123C7AA94B9D8B CRC64;

Query Match      69.8%; Score 37; DB 2; Length 4091;
Best Local Similarity 70.0%; Pred. No. 9.9e+02;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy 2 ASODIGNSLT 11
Db 3038 ASKODIGNSLT 3047

RESULT 9
KVIC_HUMAN      STANDARD;      PRT;      108 AA.
ID KVIC_HUMAN;
AC P01595;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region B1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=73029807; PubMed=4563064;
RX Braun M., Leibold W., Barnikol H.U., Hilschmann N.;
RT "Principle of antibody structure. The primary structure of a
RT monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein
RT B1). 3. The complete amino acid sequence and the genetic significance
```

RT of the variability principles for the mechanism of antibody formation."

RT Hoppe-Sejler's Z. Physiol. Chem. 353:1284-1306(1972).

CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.

CC -1- MISCELLANEOUS: This is a Bence-Jones protein.

DR HSP; P01607; 1BMV.

DR GO; GO:0005576; Cytoskeletal; NAS.

DR GO; GO:0003823; F-antigen binding; NAS.

DR GO; GO:0006855; P-immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; Ig LIKE; 1.

KM Bence-Jones protein; Direct protein sequencing;

KM Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.

AC P01645; Complementarity-determining-1.

DT 21-JUL-1986 (Rel. 01, Created)

FT DOMAIN 35 49 Framework-2.

FT DOMAIN 50 56 Complementarity-determining-2.

FT DOMAIN 57 88 Framework-3.

FT DOMAIN 89 97 Complementarity-determining-3.

FT DOMAIN 98 107 Framework-4.

FT DISULFID 23 88 By similarity.

FT NON TER 108 108

SQ SEQUENCE 108 AA; 12026 MW; 7A83983986A431E7 CRC64;

Query Match 67.9%; Score 36; DB 1; Length 108;  
Best Local Similarity 80.0%; Pred. No. 33;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASQDIGNSL 10  
:|||||  
Db 24 RASQDIRNSL 33

RESULT 10  
KVSM MOUSE  
ID KVSM MOUSE STANDARD; PRT; 108 AA.

AC P01644; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ig kappa chain V-V region HP R16.7.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxId=10090; [1]

RP SEQUENCE.

RC STRAIN=A/J; MEDLINE=82150934; PubMed=6801658;

RX Siegelman M., Capra J.D.; "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype."

RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).

CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.

CC PIR; A01927; KVSAR.

DR HSP; P01594; 1JVS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; Ig LIKE; 1.

KM Direct protein sequencing; Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.

AC P01646; Complementarity-determining-1.

DT 21-JUL-1986 (Rel. 01, Last sequence update)

FT DOMAIN 35 49 Framework-2.

FT DOMAIN 50 56 Complementarity-determining-2.

FT DOMAIN 57 88 Framework-3.

FT DOMAIN 89 97 Complementarity-determining-3.

FT DOMAIN 98 108 Framework-4.  
By similarity.

FT DISULFID 23 88

FT NON TER 108

SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFP597 CRC64;

Query Match 67.9%; Score 36; DB 1; Length 108;  
Best Local Similarity 80.0%; Pred. No. 33;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RASQDIGNSL 10  
:|||||  
Db 24 RASQDIRNSL 33

RESULT 11  
KVSL MOUSE  
ID KVSL MOUSE STANDARD; PRT; 108 AA.

AC P01645; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ig kappa chain V-V region HP 93G7.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxId=10090; [1]

RP SEQUENCE.

RC STRAIN=A/J; MEDLINE=82150934; PubMed=6801658;

RX Siegelman M., Capra J.D.; "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype."

RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).

CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.

DR HSP; P01607; 1REI.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; Ig LIKE; 1.

KM Direct protein sequencing; Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.

FT DOMAIN 35 49 Framework-2.

FT DOMAIN 50 56 Complementarity-determining-2.

FT DOMAIN 57 88 Framework-3.

FT DOMAIN 89 97 Complementarity-determining-3.

FT DOMAIN 98 108 Framework-4.

FT DISULFID 23 88 By similarity.

FT NON TER 108 108

SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFP58B CRC64;

Query Match 67.9%; Score 36; DB 1; Length 108;  
Best Local Similarity 80.0%; Pred. No. 33;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RASQDIGNSL 10  
:|||||  
Db 24 RASQDIRNSL 33

RESULT 12  
KVSM MOUSE  
ID KVSM MOUSE STANDARD; PRT; 108 AA.

AC P01646; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ig kappa chain V-V region HP 123B6.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX STRAIN=A/J;  
 RA MEDLINE=82150934; PubMed=6801658;  
 RT Siegelman M., Capra J.D.;  
 RT "Complete amino acid sequence of light chain variable regions derived  
 RT from five monoclonal anti-p-azophenylarsenate antibodies differing  
 RT with respect to a crossreactive idiotype."  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.  
 DR HSSP; P01594; 1JVS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 34 Complementarity-determining-1.  
 FT DOMAIN 35 49 Framework-2.  
 FT DOMAIN 50 56 Complementarity-determining-2.  
 FT DOMAIN 57 88 Framework-3.  
 FT DOMAIN 89 97 Complementarity-determining-3.  
 FT DOMAIN 98 108 Framework-4.  
 FT DISULFID 23 88 By similarity.  
 FT NON TER 108  
 SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08BBA09A CRC64;  
 Query Match 67.9%; Score 36; DB 1; Length 108;  
 Best Local Similarity 80.0%; Pred. No. 33;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 RASODIGNSL 10  
 Db 24 RASQDINNYL 33  
 RESULT 13  
 ID KVSQ MOUSE STANDARD; PRT; 108 AA.  
 AC P01647;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig kappa chain V-V region HP 124B1.  
 OS Mus musculus (Mouse)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX STRAIN=A/J;  
 RA MEDLINE=82150934; PubMed=6801658;  
 RT Siegelman M., Capra J.D.;  
 RT "Complete amino acid sequence of light chain variable regions derived  
 RT from five monoclonal anti-p-azophenylarsenate antibodies differing  
 RT with respect to a crossreactive idiotype."  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.  
 DR HSSP; P01607; IREI.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 34 Complementarity-determining-1.  
 FT DOMAIN 35 49 Framework-2.  
 FT DOMAIN 50 56 Complementarity-determining-2.  
 FT DOMAIN 57 88 Framework-3.

FT DOMAIN 89 97 Complementarity-determining-3.  
 FT DOMAIN 98 108 Framework-4.  
 FT DISULFID 23 88 By similarity.  
 FT NON TER 108  
 SQ SEQUENCE 108 AA; 11965 MW; 39971BC653BEEFA2 CRC64;  
 Query Match 67.9%; Score 36; DB 1; Length 108;  
 Best Local Similarity 80.0%; Pred. No. 33;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 RASODIGNSL 10  
 Db 24 RASQDINNYL 33  
 RESULT 14  
 ID KVSQ MOUSE STANDARD; PRT; 108 AA.  
 AC P01648;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig kappa chain V-V region HP 91A3.  
 OS Mus musculus (Mouse)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX STRAIN=A/J;  
 RA MEDLINE=82150934; PubMed=6801658;  
 RT Siegelman M., Capra J.D.;  
 RT "Complete amino acid sequence of light chain variable regions derived  
 RT from five monoclonal anti-p-azophenylarsenate antibodies differing  
 RT with respect to a crossreactive idiotype."  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.  
 DR HSSP; P01594; 1JVS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 34 Complementarity-determining-1.  
 FT DOMAIN 35 49 Framework-2.  
 FT DOMAIN 50 56 Complementarity-determining-2.  
 FT DOMAIN 57 88 Framework-3.  
 FT DOMAIN 89 97 Complementarity-determining-3.  
 FT DOMAIN 98 108 Framework-4.  
 FT DISULFID 23 88 By similarity.  
 FT NON TER 108  
 SQ SEQUENCE 108 AA; 11961 MW; D52EDA5B9A45291C CRC64;  
 Query Match 67.9%; Score 36; DB 1; Length 108;  
 Best Local Similarity 80.0%; Pred. No. 33;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 RASODIGNSL 10  
 Db 24 RASQDINNYL 33  
 RESULT 15  
 ID Q925S9 PRELIMINARY; PRT; 127 AA.  
 AC Q925S9;  
 DT 01-DEC-2001 (TRMBLrel. 19, Created)  
 DT 01-DEC-2001 (TRMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)  
 DE Immunoglobulin light chain (Fragment).  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OK NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=99306687; PubMed=10380019;  
 RA Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,  
 RA Feon K.A., Chatterjee S.K.;  
 RT "Construction and characterization of a chimeric fusion protein  
 RT consisting of an anti-idiotypic antibody mimicking a breast cancer-  
 RT associated antigen and the cytokine GM-CSF."  
 RL Hybridoma 18:193-202(1999).  
 DR EMBL; AF124721; AAK55120.1; -.  
 DR HSSP; P01594; IUV5.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON TER 127 127  
 SQ SEQUENCE 127 AA; 13794 MW; 13F61BBB981FA5 CRC64;

Query Match 67.9%; Score 36; DB 2; Length 127;  
 Best Local Similarity 80.0%; Pred. No. 40;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10  
 DB 44 RASQDIGINL 53

Search completed: April 4, 2005, 15:56:08  
 Job time : 20.5911 secs



CC entero, polio, influenza or immune deficiency viruses  
XX Sequence 7 AA;  
SQ

Query Match 100.0%; Score 31; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7  
DB 1 ATSSLDS 7

## RESULT 2

AAV44590  
ID AAV44590 standard; protein; 7 AA.

AC AAV44590;

DT 04-APR-2000 (first entry)

XX Mouse anti-IL-18 antibody VL complementarity-determining region-2.

XX Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;

KM complementarity-determining region; CDR; hybridoma #125-2H; mouse;

KM monoclonal antibody #125-2Hmab; interleukin-18; antiinflammatory;

KM immunosuppressive; leucocytopenic; antiallergic; antipyretic;

KM antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy;

XX inflammatory disorder; immunoreaction.

XX Mus musculus.

OS EP974600-A2.

PN 26-JUN-2000.

PD 24-JUN-1999; 99EP-00304977.

PF 24-JUN-1998; 98JP-00177580.

PR 12-OCT-1998; 98JP-00289044.

PR 22-DEC-1998; 98JP-00365023.

XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.

XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX WPI; 2000-118341/11.

DR N-PSDB; AA249537.

XX New artificially produced peptide for neutralizing biological activity of

PT interleukin-18, useful for treating and preventing immunopathies,

PT inflammatory disorders and autoimmune diseases.

XX Claim 7, Page 18; 32pp; English.

XX The present protein sequence is a complementarity-determining region

CC (CDR) of mouse anti-Interleukin-18 antibody light chain variable region

CC (VL) encoded by cDNA derived from hybridoma #125-2H. The nucleotide

CC sequence can be used in the production of recombinant monoclonal antibody

CC #125-2Hmab, which is capable of neutralizing biological activities of

CC interleukin-18. The antibody has antinflammatory, immunosuppressive,

CC leucocytopenic, antiallergic, antipyretic, antiallergic and hepatotropic

CC activity and can be used for prevention and treatment of autoimmune

CC diseases, immunopathies and inflammatory disorders caused by excessive

CC immunoreaction

XX Sequence 7 AA;  
SQ

DB 1 ATSSLDS 7

Query Match 100.0%; Score 31; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7  
DB 1 ATSSLDS 7

## RESULT 3

ABR55316  
ID ABR55316 standard; peptide; 7 AA.

AC ABR55316;

DT 29-JUL-2003 (first entry)

XX Complementarity determining region of light chain of antibody VR165.

XX Antibody; kinase insert domain-containing receptor; KDR; antibody VR165;

KM complementarity determining region; vascular endothelial growth factor;

KM CDR; VEGF; inflammation; psoriasis; rheumatoid arthritis; tumour.

XX Mus sp.

OS WO2003031475-A2.

PN 17-APR-2003.

PD 10-OCT-2002; 2002WO-GB004619.

PR 10-OCT-2001; 2001GB-00024317.

PR (CELL-) CELLTECH R & D LTD.

XX Popplewell AG, Tickle SP, Zinkewich-Peotti K, Morrison RK;

XX WPI; 2003-441133/41.

DR Novel antibody molecules having specificity for human kinase insert

XX domain-containing receptors, useful for treating inflammation, psoriasis,

XX rheumatoid arthritis, tumor growth and metastasis.

XX Claim 2, Fig 1; 57pp; English.

XX The specification describes an antibody molecule which has specificity

CC for human kinase insert domain-containing receptor (KDR). The antibody

CC comprises complementarity determining regions (CDRs) from the heavy and

CC light chain variable domains of the murine monoclonal antibody VR165.

CC This antibody is specific for human KDR. The antibody of the invention

CC blocks vascular endothelial growth factor (VEGF) binding to KDR.

CC Antibodies of the invention are useful for treating a pathology in which

CC VEGF and/or KDR are implicated, and in the manufacture of a medicament

CC for the treatment of a pathology in which VEGF and/or KDR are implicated.

CC This includes inflammation, psoriasis, rheumatoid arthritis, and tumour

CC growth or metastasis. ABR55315-17 represent the CDRs of the light chain

CC variable region of VR165 antibody. They are used to produce antibodies of

CC the invention

XX Sequence 7 AA;  
SQ

## RESULT 4

ADM78136  
ID ADM78136 standard; peptide; 7 AA.

AC ADM78136;

DT 01-JUL-2004 (first entry)

XX Novel antibody molecules having specificity for human kinase insert

XX domain-containing receptors, useful for treating inflammation, psoriasis,

XX rheumatoid arthritis, tumor growth and metastasis.

XX Claim 2, Fig 1; 57pp; English.

XX The specification describes an antibody molecule which has specificity

CC for human kinase insert domain-containing receptor (KDR). The antibody

CC comprises complementarity determining regions (CDRs) from the heavy and

CC light chain variable domains of the murine monoclonal antibody VR165.

CC This antibody is specific for human KDR. The antibody of the invention

CC blocks vascular endothelial growth factor (VEGF) binding to KDR.

CC Antibodies of the invention are useful for treating a pathology in which

CC VEGF and/or KDR are implicated, and in the manufacture of a medicament

CC for the treatment of a pathology in which VEGF and/or KDR are implicated.

CC This includes inflammation, psoriasis, rheumatoid arthritis, and tumour

CC growth or metastasis. ABR55315-17 represent the CDRs of the light chain

CC variable region of VR165 antibody. They are used to produce antibodies of

CC the invention

XX Sequence 7 AA;  
SQ

DE Human SUB3-86 antibody variable light chain CDR2 peptide region.  
XX  
XX monoclonal antibody; adenylate kinase isozyme 3;  
KM complementarity determining region; CDR; heart disease; marker AK3;  
KW biochemical; human; variable; light chain.  
XX  
XX Homo sapiens.  
OS  
XX WO2004029094-A1.  
PN  
XX  
XX 08-APR-2004.  
PD  
XX 27-SEP-2003; 2003WO-KR001979.  
PF  
XX 28-SEP-2002; 2002KR-00059211.  
PR  
XX (KIMH/) KIM H.  
PA  
XX KIM H;  
PI  
XX WPI; 2004-316088/29.  
DR  
XX  
XX New monoclonal antibody specific to human mitochondrial adenylate kinase  
PT isozyme 3, useful for preparing a composition for detecting a heart  
PT disease marker AK3.  
PS  
XX Claim 1; SEQ ID NO 99; 126pp; English.  
XX  
XX The invention relates to a novel monoclonal antibody specific to  
CC adenylate kinase isozyme 3, comprising 4 or more of 6 complementarity  
CC determining regions (CDRs) of a sequence having 6-18 amino acids. The  
CC invention further relates to: a composition comprising the monoclonal  
CC antibody for detecting a heart disease marker AK3; a kit comprising the  
CC monoclonal antibody for the diagnosis of heart disease; and a method of  
CC detecting a heart disease marker AK3. The monoclonal antibody is useful  
CC for preparing a composition for detecting a heart disease marker AK3. The  
CC monoclonal antibody reduces false positive results of the conventional  
CC biochemical markers. This sequence represents a human antibody variable  
CC light chain CDR peptide region of the invention.  
CC  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 31; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ATSSLDS 7  
DB 1 ATSSLDS 7  
RESULT 5  
ADO60479  
ID ADO60479 standard; peptide; 7 AA.  
AC ADO60479;  
XX  
XX 12-AUG-2004 (first entry)  
DT  
XX  
DE Mouse antibody 83-14 light chain CDR2.  
XX  
XX neuroprotective; targeted therapy; humanised antibody;  
KM human insulin receptor; HIR; heavy chain; constant region;  
KW variable region; complementarity determining region; CDR; framework;  
KW neuropharmaceutical agent; blood brain barrier; avidin-biotin linkage;  
KW mouse; antibody 83-14; Mab 83-14; light chain variable region; VL; CDR.  
XX  
XX Mus sp.  
OS  
XX US2004101904-A1.  
PN  
XX 27-MAY-2004.  
PD  
XX

PF 27-NOV-2002; 2002US-00307276.  
XX  
XX 27-NOV-2002; 2002US-00307276.  
PR  
XX  
XX (REGC ) UNIV CALIFORNIA.  
PA  
XX  
XX Partridge WM, Bado RJ;  
PI  
XX WPI; 2004-459888/43.  
DR  
XX  
XX Humanized murine antibody that bind to human insulin receptor useful to  
PT transport neuropharmaceutical agents; has heavy and light amino acid  
PT chain having complementarity determining regions interspersed between  
PT humanized framework regions.  
PS  
XX Claim 2; SEQ ID NO 40; 34pp; English.  
XX  
XX The invention describes a humanised antibody (I) that binds with the  
CC human insulin receptor (HIR). The humanised antibody comprises a heavy  
CC chain of amino acids comprising a constant region and a variable region  
CC where the variable region has an amino end and a carboxyl end and  
CC comprises complementarity determining regions (CDR) interspersed between  
CC framework regions, the CDR comprises a first CDR located at the amino end  
CC of the variable region, a third CDR located at the carboxyl end of the  
CC variable region and a second CDR located between the first and third  
CC CDRs. The framework regions comprise a first frame work region located  
CC adjacent to the amino end of the first CDR, a second framework region  
CC located between the first and second CDR, a third frame work region  
CC located between the second and third CDR and a fourth frame work region  
CC located adjacent to the carboxyl end of the third CDR, where the  
CC framework regions have been humanized, and a light chain of aminoacids  
CC compatible with the heavy chain. (I) is useful for increasing the ability  
CC of neuropharmaceutical agent to cross the human blood brain barrier which  
CC involves linking the neuropharmaceutical agent to (I) by an avidin-biotin  
CC linkage or by genetic fusion. (I) is useful for targeting a  
CC pharmaceutical agent to the HIR in vivo which involves linking the  
CC pharmaceutical agent to (I). A preparation (II) comprising (I) is useful  
CC for intravenously administering a pharmaceutical agent to a human patient  
CC which involves injecting (II) into blood stream of the human patient. (I)  
CC is useful in combination with drug and diagnostic agent to treat human  
CC beings in vivo. (I) is useful as Trojan horse to transport  
CC neuropharmaceutical agents across blood brain barrier. This is the amino  
CC acid sequence of mouse antibody 83-14 light chain complementarity  
CC determining region 2 (CDR2), showing the preferred sequence of the CDR  
CC within the humanised antibody.  
CC  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 31; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ATSSLDS 7  
DB 1 ATSSLDS 7  
RESULT 6  
ABR55336  
ID ABR55336 standard; peptide; 30 AA.  
AC ABR55336;  
XX  
XX 29-JUL-2003 (first entry)  
DT  
XX  
DE Amino acid sequence of cassette used to construct a light chain graft.  
XX  
XX Antibody; kinase insert domain-containing receptor; KDR; antibody VR165;  
KM complementarity determining region; vascular endothelial growth factor;  
KW CDR; VEGF; inflammation; psoriasis; rheumatoid arthritis; tumour.  
XX  
XX  
OS  
XX Synthetic.  
PD  
XX

PN WO2003031475-A2.  
 XX 17-APR-2003.  
 XX  
 XX 10-OCT-2002; 2002WO-GB004619.  
 XX  
 XX 10-OCT-2001; 2001GB-00024317.  
 XX  
 XX (CELL-) CELUTECH R & D LTD.  
 XX  
 XX Popplewell AG, Tickle SP, Zinkewich-Beotti K, Morrison RK;  
 XX  
 XX WPI; 2003-441133/41.  
 XX  
 XX N-PSDB; ACCT0039.  
 XX  
 XX Novel antibody molecules having specificity for human kinase insert  
 PT domain-containing receptors, useful for treating inflammation, psoriasis,  
 PT rheumatoid arthritis, tumor growth and metastasis.  
 XX  
 XX Example; Fig 13; 57pp; English.  
 XX  
 XX The specification describes an antibody molecule which has specificity  
 CC for human kinase insert domain-containing receptor (KDR). The antibody  
 CC comprises complementarily determining regions (CDRs) from the heavy and  
 CC light chain variable domains of the murine monoclonal antibody VRI65.  
 CC This antibody is specific for human KDR. The antibody of the invention  
 CC blocks vascular endothelial growth factor (VEGF) binding to KDR.  
 CC Antibodies of the invention are useful for treating a pathology in which  
 CC VEGF and/or KDR are implicated, and in the manufacture of a medicament  
 CC for the treatment of a pathology in which VEGF and/or KDR are implicated.  
 CC This includes inflammation, psoriasis, rheumatoid arthritis, and tumour  
 CC growth or metastasis. The present sequence represents a cassette used to  
 CC construct optimised heavy chain grafts, for production of antibody  
 CC molecules of the invention  
 XX  
 XX Sequence 30 AA;  
 SQ  
 Query Match 100.0%; Score 31; DB 6; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATSSIDS 7  
 DB 1 ATSSIDS 7  
 RESULT 7  
 ADM91687  
 ID ADM91687 standard; protein; 83 AA.  
 XX  
 XX ADM91687;  
 AC  
 XX  
 XX 15-JUL-2004 (first entry)  
 DT  
 XX  
 XX Lawsonia intracellularis specific amino acid sequence SEQ ID NO:88.  
 DB  
 XX  
 XX Lawsonia intracellularis; infection; antibacterial; immunotherapy;  
 KM proliferative enteropathy.  
 XX  
 XX Lawsonia intracellularis.  
 OS  
 XX  
 XX WO2004033631-A2.  
 PN  
 XX  
 XX 22-APR-2004.  
 PD  
 XX  
 XX 01-OCT-2003; 2003WO-US031318.  
 PF  
 XX  
 XX 04-OCT-2002; 2002US-0416395P.  
 PR  
 XX  
 XX (MINU ) UNIV MINNESOTA.  
 PA  
 XX  
 XX Kapur V, Gebhart CJ;  
 PI  
 XX

DR WPI; 2004-340902/31.  
 DR N-PSDB; ADM91625.  
 XX  
 XX New nucleic acid that generates an amplification product from L.  
 PT intracellularis nucleic acid using an appropriate second nucleic acid  
 PT molecule, useful for treating and preventing L. intracellularis  
 PT infection.  
 XX  
 XX Disclosure; SEQ ID NO 88; 87pp; English.  
 XX  
 XX The present invention describes an isolated nucleic acid comprising a  
 CC nucleic acid molecule of at least 10 nucleotides in length having at  
 CC least 75% identity to SEQ ID NO:8741 (ADM91733), where any of the  
 CC molecule that is 10-29 nucleotides in length, under standard  
 CC amplification conditions, generates an amplification product from  
 CC Lawsonia intracellularis nucleic acid using an appropriate second nucleic  
 CC acid molecule. Also described: (1) a vector comprising the nucleic acid;  
 CC (2) a host cell comprising the vector; (3) an isolated polypeptide  
 CC encoded by the nucleic acid; (4) an article of manufacture comprising the  
 CC polypeptide; (5) an antibody having specific binding affinity for the  
 CC polypeptide; (6) a method for detecting the presence or absence of L.  
 CC intracellularis in a biological sample; (7) a method of preventing  
 CC infection by L. intracellularis in an animal; (8) a composition  
 CC comprising a first oligonucleotide primer and a second oligonucleotide  
 CC primer, where the first and second primers are each 10 to 50 nucleotides  
 CC in length, and where in the presence of L. intracellularis nucleic acid,  
 CC generate an amplification product under standard amplification  
 CC conditions, but do not generate an amplification product in the presence  
 CC of nucleic acid from an organism other than L. intracellularis; and (9)  
 CC an article of manufacture comprising the composition. The nucleic acid  
 CC sequence has antibacterial activity, and can be used in immunotherapy.  
 CC The nucleic acid and polypeptides are useful for treating and preventing  
 CC L. intracellularis infection e.g. proliferative enteropathy. The present  
 CC sequence represents an L. intracellularis specific amino acid sequence,  
 CC which is used in the exemplification of the present invention.  
 XX  
 XX Sequence 83 AA;  
 SQ  
 Query Match 100.0%; Score 31; DB 8; Length 83;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATSSIDS 7  
 DB 6 ATSSIDS 12  
 RESULT 8  
 AAR80078  
 ID AAR80078 standard; protein; 90 AA.  
 XX  
 XX AAR80078;  
 AC  
 XX  
 XX 22-MAY-1996 (first entry)  
 DT  
 XX  
 XX Mouse derived light chain RT3 phage antibody pattern A.  
 DE  
 XX  
 XX Light chain; RT3; murine; catalytic antibody; bacteriophage; pattern A.  
 KM  
 XX  
 XX Mus musculus.  
 OS  
 XX  
 XX Key  
 FT 1..15 Location/Qualifiers  
 FT Region  
 FT /note= "framework region 1"  
 FT 16..26  
 FT /note= "complementarity determining region 1"  
 FT 27..40  
 FT /note= "framework region 2"  
 FT 41..47  
 FT /note= "complementarity determining region 2"  
 FT 48..78  
 FT /note= "framework region 3"  
 FT 79..88  
 FT Region

/note= "complementarity determining region 3"  
89..90  
/note= "framework region 4 N-terminal fragment"

FT Region  
FT 89..90  
XX /note= "framework region 4 N-terminal fragment"  
XX W09527045-A1.  
XX  
XX  
XX 12-OCT-1995.  
XX  
XX 30-MAR-1994; 94WO-US003420.  
XX  
XX 30-MAR-1994; 94WO-US003420.  
XX  
XX 30-MAR-1994; 94WO-US003420.  
XX  
XX (IGEN-) IGEN INC.  
XX  
XX Smith RG, Mccafferty J, Chiswell D, Darsley MJ, Fitzgerald K,  
PI Kenten JH, Martin MT, Titmas RC, Williams RO,  
XX  
XX WPI, 1995-358624/46.  
XX N-PSDB; AAT04625.  
XX  
XX Production of catalytic antibodies displayed on phage - by generating a  
PT gene library of antibody-derived domains and expressing it in phage  
PT vectors.  
XX  
XX Disclosure; Fig 9; 133pp; English.  
XX  
XX AAT04625 encodes AAR8078 mouse derived light chain RT3 phage antibody.  
CC The DNA was used in the prepn. of catalytic antibody (CA) producing  
CC bacteriophage. The CA's can be used to activate/deactivate a biological  
CC function in an animal by enhancing the rate of cleavage, or formation of  
CC a specific bond within a mol. in vivo  
XX  
XX Sequence 90 AA;  
SQ

Query Match 100.0%; Score 31; DB 2; Length 90;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATSSLDS 7  
|||  
41 ATSSLDS 47

RESULT 9  
AAW95480  
ID AAW95480 standard; protein; 92 AA.  
XX  
XX AAW95480;  
AC

XX 29-MAR-1999 (first entry)  
DT

XX Mouse derived RT3 phage antibody light chain pattern C genetic sequence.  
DE  
XX Catalytic; antibody; phage display; immunising; phage expression vector;  
KM prodnug; scfv.  
XX  
XX Mus sp.  
OS

XX US5855885-A.  
PN  
XX 05-JAN-1999.  
PD  
XX 14-JUL-1994; 94US-00273146.  
PF  
XX 22-JAN-1993; 93US-00007684.  
PR  
XX

XX (MCCA/) MCCAFFERTY J.  
PA (CHIS/) CHISWELL D.  
PA (DARS/) DARSLEY M J.  
PA (TITM/) TITMAS R C.  
PA (MART/) MARTIN M T.  
PA (KENT/) KENTEN J H.  
PA (SMIT/) SMITH R.

PA (FITZ/) FITZGERALD K.  
PA (WILL/) WILLIAMS R O.  
XX  
XX Fitzgerald K, Darsley MJ, Williams RO, Smith R, Martin MT;  
PI Kenten JH, Chiswell D, Mccafferty J, Titmas RC;  
XX  
XX WPI, 1999-105036/09.  
XX N-PSDB; AAX00879.  
DR  
XX  
XX Production of catalytic antibodies displayed on bacteriophages -  
PT comprises generating a gene library of antibody-derived domains inserting  
PT coding into a phage expression vector and isolating the catalytic  
PT antibodies.  
XX  
XX Example 4; Fig 11; 117pp; English.  
XX  
XX

CC The invention relates to methods for producing catalytic antibodies  
CC displayed on a phage. The method comprises: (a) generating a gene library  
CC of antibody-derived domains; (b) inserting coding for the domains into a  
CC phage expression vector; and (c) isolating the catalytic antibodies. The  
CC phage expression vector incorporates a histidine peptide in tandem with a  
CC myc peptide. The catalytic antibodies can be isolated by preparing an  
CC antigen; optionally immunising an animal with the antigen; generating a  
CC library of VH and VL domains from the immunised animal; cloning the VH  
CC and VL domains into a phage expression vector to generate phage display  
CC antibodies; selecting phage display antibodies which bind specifically to  
CC the antigen; screening the selected phage display antibodies for  
CC catalytic activity to substrate; and isolating the catalytic antibodies,  
CC where the phage expression vector incorporates a histidine peptide in  
CC tandem with a myc peptide. The processes are used to produce catalytic  
CC antibodies, which can be used for in vivo activation of a prodnug. The  
CC present sequence represents a genetic sequence of light chain PCR pattern  
CC C from mouse derived RT3 phage antibodies  
XX  
XX Sequence 92 AA;  
SQ

Query Match 100.0%; Score 31; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATSSLDS 7  
|||  
42 ATSSLDS 48

RESULT 10  
AAW95476  
ID AAW95476 standard; protein; 92 AA.  
XX  
XX AAW95476;  
AC

XX 29-MAR-1999 (first entry)  
DT

XX Mouse derived RT3 phage antibody light chain pattern A genetic sequence.  
DE  
XX Catalytic; antibody; phage display; immunising; phage expression vector;  
KM prodnug; scfv.  
XX  
XX Mus sp.  
OS

XX US5855885-A.  
PN  
XX 05-JAN-1999.  
PD  
XX 14-JUL-1994; 94US-00273146.  
PF  
XX 22-JAN-1993; 93US-00007684.  
PR  
XX

XX (MCCA/) MCCAFFERTY J.  
PA (CHIS/) CHISWELL D.  
PA (DARS/) DARSLEY M J.  
PA (TITM/) TITMAS R C.  
PA (MART/) MARTIN M T.

PA (KENT/) KENTEN J H.  
PA (SMIT/) SMITH R.  
PA (FITZ/) FITZGERALD K.  
PA (WILL/) WILLIAMS R O.  
XX  
PI Fitzgerald K, Daraley MJ, Williams RO, Smith R, Martin MT;  
PI Kenten JH, Chiswell D, Mc Cafferty J, Tiltmas RC;  
XX  
DR WPI; 1999-105036/09.  
DR N-PSDB; AAX00875.  
XX  
PT Production of catalytic antibodies displayed on bacteriophages -  
PT comprises generating a gene library of antibody-derived domains inserting  
PT coding into a phage expression vector and isolating the catalytic  
PT antibodies.  
XX  
XX  
PS Example 4; Fig 9A-F; 117pp; English.  
XX  
CC The invention relates to methods for producing catalytic antibodies  
CC displayed on a phage. The method comprises: (a) generating a gene library  
CC of antibody-derived domains; (b) inserting coding for the domains into a  
CC phage expression vector; and (c) isolating the catalytic antibodies. The  
CC phage expression vector incorporates a histidine peptide in tandem with a  
CC myc peptide. The catalytic antibodies can be isolated by preparing an  
CC antigen; optionally immunising an animal with the antigen; generating a  
CC library of VH and VL domains from the immunised animal; cloning the VH  
CC and VL domains into a phage expression vector to generate phage display  
CC antibodies; selecting phage display antibodies which bind specifically to  
CC the antigen; screening the selected phage display antibodies for  
CC catalytic activity to substrate; and isolating the catalytic antibodies,  
CC where the phage expression vector incorporates a histidine peptide in  
CC tandem with a myc peptide. The processes are used to produce catalytic  
CC antibodies, which can be used for in vivo activation of a prodruq. The  
CC present sequence represents a genetic sequence of light chain pattern A  
CC from mouse derived R13 phage antibodies  
XX  
SQ Sequence 92 AA;  
  
Query Match 100.0%; Score 31; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATSSIDS 7  
DB 42 ATSSIDS 48  
  
RESULT 11  
AAW70954  
ID AAW70954 standard; protein; 95 AA.  
XX  
AC AAW70954;  
XX  
DT 14-OCT-1998 (first entry)  
XX  
DE Light chain of monoclonal antibody RS-255.  
XX  
XX Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;  
KM respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;  
KM viral infection; inhibit; fusion; protection; transcription;  
KM antiviral agent; prophylaxis; diagnosis; infection; contamination.  
XX  
OS Mus sp.  
XX  
PN FR2758331-A1.  
XX  
PD 17-JUL-1998.  
XX  
PF 14-JAN-1997; 97FR-00000300.  
XX  
PR 14-JAN-1997; 97FR-00000300.  
XX  
PA (UYBO-) UNITV BOURGOGNE.

XX  
DR WPI; 1998-390320/34.  
XX  
XX  
PT New peptide(s) recognising viral epitope with tropism to mucosa - useful  
PT for, e.g. diagnosing, preventing and treating viral infection(s).  
XX  
PS Disclosure; Fig 2; 51pp; French.  
XX  
CC  
CC The present sequence represents the light chain of monoclonal antibody RS  
CC -255, which is directed against the respiratory syncytial virus (RSV).  
CC The specification describes peptides which recognise, by antigen-antibody  
CC type reactions, at least 1 epitope of a pathogenic virus having tropism  
CC for the mucosa. AAW70905-16 and AAW70923-46 are analogous to CDR regions  
CC of monoclonal antibodies specific for RSV. AAW70917-28 are analogous to  
CC CDR regions of monoclonal antibodies specific for site III or IV of the  
CC VP6 protein of rota virus (RV). The peptides can neutralise viral  
CC infections and may also inhibit fusion between infected and uninfected  
CC cells or cells and viruses. They provide passive or active protection  
CC and/or inhibit transcription of the virus, so are useful as antiviral  
CC agents or for prophylaxis, in human or veterinary medicine. The peptides  
CC can be labelled and used to diagnose infection or contamination by the  
CC virus. The peptides are particularly directed against RSV or RS but may  
CC also be used against papilloma, adeno, entero, polio, influenza or immune  
CC deficiency viruses  
XX  
SQ Sequence 95 AA;  
  
Query Match 100.0%; Score 31; DB 2; Length 95;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATSSIDS 7  
DB 37 ATSSIDS 43  
  
RESULT 12  
ABP33764  
ID ABP33764 standard; protein; 97 AA.  
XX  
AC ABP33764;  
XX  
DT 08-JUL-2002 (first entry)  
XX  
DE Human transport protein-like ORF2737 protein, SEQ ID NO:5474.  
XX  
XX Human; ORF; open reading frame; ORF; drug screening; diagnosis;  
KM disease monitoring; cytokine; cell proliferation; cell differentiation;  
KM immune modulation; haematopoiesis regulation; tissue growth;  
KM angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;  
KM thrombolytic; tumour inhibition; bodily characteristics; fertility;  
KM behaviour; cancer; proliferative disorder; neurological disorder;  
KM cardiovascular disease; immune system disorder; organ transplantation;  
KM tissue growth disorder; tissue regeneration disorder; diabetes mellitus;  
KM hypothyroidism; cholesterol ester storage disease; infection; vulnery;  
KM neurotropic; antiporiatic; antidiabetic; cytostatic; noctropic;  
KM neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;  
KM cardiac; hypotensive; antichyroid; antinflammatory; immunomodulator;  
KM dermatological; analgesic; vitrucide; antibacterial; fungicide.  
XX  
OS Homo sapiens.  
XX  
PN WO200190366-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US017076.  
XX  
PR 24-MAY-2000; 2000US-0206690P.  
XX  
PA (CIRA-) CURAGEN CORP.  
XX  
PI Leach MD, Shinkets RA;



```

XX DR MPI: 2002-106200/14.
XX DR N-PSDB; ABR77790.
XX PT Novel human polypeptides and polynucleotides useful for diagnosing,
XX PT preventing and treating cardiovascular disease, neurodegenerative,
XX PT hyperproliferative disorders and disorders related to organ
XX PT transplantation.
XX PS Claim 10; Page 1619-1620; 2508pp; English.
XX
CC Sequences ABP31028-ABP35561 represent 4534 novel human proteins
CC designated ORF (open reading frame) 1-4534, and sequences ABR75054-
CC ABR79587 represent cDNAs encoding them. The invention also encompasses
CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
CC polynucleotides, the recombinant production of ORFX proteins, antibodies
CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
CC polypeptides, methods of screening for modulators of ORFX expression or
CC activity, and methods of screening individuals for a predisposition to an
CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
CC range of biological activities, such as cytokine, cell proliferation,
CC cell differentiation, immune modulation, haematopoiesis regulation,
CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic activity, tumour inhibition activity,
CC receptor/ligand, anti-inflammatory activity, tumour inhibition activity,
CC and anti-infective activity, and may also be involved in the determination
CC of bodily characteristics, fertility and behaviour. ORFX proteins,
CC nucleic acids and antibodies may be used in the treatment of cancers,
CC other proliferative disorders such as psoriasis and benign tumours,
CC neurological disorders such as epilepsy and Alzheimer's disease,
CC cardiovascular diseases, immune system disorders, disorders related to
CC organ transplantation, disorders of tissue growth and regeneration,
CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
CC storage disease, and infectious diseases caused by viral, bacterial,
CC fungal and other pathogens. ORFX nucleic acids may also be used as a
CC source of primers and probes, in the detection of ORFX genomic sequences
CC or transcripts, in the identification and cloning of homologous
CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
CC nucleic acids may additionally be used to produce transgenic animals
CC which may be useful for studying the function and/or activity of ORFX
CC protein, and in drug screening. The ORFX proteins may also be used as
CC immunogens to generate specific antibodies, which are useful in the
CC diagnosis, treatment and monitoring of ORFX-associated diseases
CC
XX SQ Sequence 97 AA:

```

```

Query Match      100.0%; Score 31; DB 5; Length 97;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 ATSSDS 7
   |||||
Db 52 ATSSDS 58

```

```

RESULT 13
ADM78077
ID ADM78077 standard; protein; 99 AA.
XX ADM78077;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human 5A3-86 antibody variable light chain region, SEQ ID NO 40.
XX
XX monoclonal antibody; adenylate kinase isozyme 3;
XX complementary determining region; CDR; heart disease; marker AK3;
XX biochemical; human; variable; light chain.
XX
XX Homo sapiens.
XX

```

```

PN WO2004029094-A1.
XX
XX PD 08-APR-2004.
XX
XX PF 27-SEP-2003; 2003WO-KR001979.
XX
XX PR 28-SEP-2002; 2002KR-00059211.
XX
XX (KIMH/) KIM H.
XX
XX Kim H;
XX
XX DR MPI: 2004-316088/29.
XX DR N-PSDB; ADM78076.
XX
XX PT New monoclonal antibody specific to human mitochondrial adenylate kinase
XX PT isozyme 3, useful for preparing a composition for detecting a heart
XX PT disease marker AK3.
XX
XX PS Example 5; SEQ ID NO 40; 126pp; English.
XX
XX CC The invention relates to a novel monoclonal antibody specific to
XX CC adenylate kinase isozyme 3, comprising 4 or more of 6 complementarity
XX CC determining regions (CDRs) of a sequence having 6-18 amino acids. The
XX CC invention further relates to: a composition comprising the monoclona
XX CC antibody for detecting a heart disease marker AK3; a kit comprising the
XX CC monoclona antibody for the diagnosis of heart disease; and a method of
XX CC detecting a heart disease marker AK3. The monoclona antibody is useful
XX CC for preparing a composition for detecting a heart disease marker AK3. The
XX CC monoclona antibody reduces false positive results of the conventional
XX CC biochemical markers. This sequence represents a human variable light
XX CC chain region protein of the invention.
XX
XX SQ Sequence 99 AA:

```

```

Query Match      100.0%; Score 31; DB 8; Length 99;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ATSSDS 7
   |||||
Db 41 ATSSDS 47

```

```

RESULT 14
AAW27121
ID AAW27121 standard; protein; 107 AA.
XX
XX AAW27121;
XX
XX 25-MAR-2003 (revised)
XX DT 04-JAN-1998 (first entry)
XX
XX Murine antibody light chain variable region consensus.
XX
XX Monoclona antibody 11D10; anti-idiotype antibody; mucin;
XX KW human milk fat globule; HMEG; tumour; breast cancer; vaccine.
XX
XX Mus musculus.
XX
XX
XX Key Location/Qualifiers
XX FT 24..34
XX FT /label= CDR1
XX FT /note= "complementarity determining region 1"
XX FT 50..56
XX FT /label= CDR2
XX FT /note= "complementarity determining region 2"
XX FT 88..96
XX FT /label= CDR3
XX FT /note= "complementarity determining region 3"
XX
XX WO9722699-A2.
XX

```

PD 26-JUN-1997.  
 XX  
 PF 19-DEC-1996; 96WO-US020757.  
 XX  
 PR 20-DEC-1995; 95US-00575762.  
 PR 26-JAN-1996; 96US-00591965.  
 PR 13-DEC-1996; 96US-00766350.  
 XX  
 PA (KENT ) UNIV KENTUCKY.  
 PI Chatterjee M, Foon KA, Chatterjee SK.  
 DR WPI; 1997-341690/31.  
 XX  
 PT Monoclonal anti-idiotypic antibody 11D10 - elicits immune response against  
 human milk fat globule disease associated tumours, especially breast  
 cancer.  
 PS Example 2; Fig 26C; 130pp; English.  
 XX  
 CC This polypeptide sequence comprises a consensus sequence of murine light  
 chain variable regions (VL) selected on the basis of identity to the VL  
 region (see W27119) of monoclonal anti-idiotypic antibody 11D10. The  
 CC sequences were obtained from a GenBank database search. A VH consensus  
 CC (W27122) was also produced. 11D10 has at least 18 departures from the  
 CC consensus sequences (7 in the light chain and 11 in the heavy chain). 8  
 CC occur within CDRs and 10 outside CDRs. 11D10 polypeptides and  
 CC polynucleotides can be used in vaccines and pharmaceutical compositions  
 CC for the treatment of human milk fat globule-associated diseases such as  
 CC breast cancer. (Updated on 25-MAR-2003 to correct PR field.)  
 CC  
 SQ Sequence 107 AA;

Query Match 100.0%; Score 31; DB 2; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
 |||||  
 Db 50 ATSSIDS 56

RESULT 15

AA90824  
 ID AAY90824 standard; protein; 107 AA.

XX  
 AC AAY90824;

XX  
 DT 29-AUG-2000 (first entry)

XX  
 DE 520C9 hybridoma VL domain SEQ ID NO:26.

XX  
 KW Antigen binding site; immunoglobulin; cancer antigen; immunological;  
 antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;

KW specific binding assay; affinity purification; drug targeting;  
 KW toxin targeting; imaging; genetic; therapeutic.

XX  
 OS Homo sapiens.

XX  
 PN US6054561-A.

XX  
 PD 25-APR-2000.

XX  
 PF 07-JUN-1995; 95US-00483749.

XX  
 PR 08-FEB-1984; 84US-00577976.

PR 11-JAN-1985; 85US-00690750.

PR 21-MAR-1986; 86US-00842476.

PR 08-MAY-1988; 88US-00190778.

PR 11-AUG-1994; 94US-00288981.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX

PI Ring DB;  
 XX  
 DR WPI; 2000-338508/29.  
 DR N-PSDB; AAA38908.  
 XX  
 PT Monoclonal antibody capable of binding to human breast cancer antigen  
 useful for affinity purification, drug or toxin targeting, imaging, and  
 PT treating cancer.  
 PS Disclosure; Fig 13; 57pp; English.  
 XX  
 CC The present invention describes a monoclonal antibody (Mab) (I) that  
 CC binds to a human breast cancer antigen that is also bound by Mab 454C11  
 CC and 520C9 (produced by hybridoma ATCC HB8484 and HB8696, respectively). Also  
 CC described is a hybridoma that produces (I). (I) is useful in specific  
 CC binding assays, affinity purification, drug or toxin targeting, imaging,  
 CC and genetic or immunological therapeutics for various cancers. The  
 CC present sequence represents a VL domain derived from a 520C9 hybridoma,  
 CC which is used in the exemplification of the present invention

SQ Sequence 107 AA;

Query Match 100.0%; Score 31; DB 3; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
 |||||  
 Db 50 ATSSIDS 56

Search completed: April 4, 2005, 15:47:17  
 Job time : 15.9776 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 10.3323 Seconds  
(without alignments)  
224.651 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_183\_189

Perfect score: 31

Sequence: 1 ATSSIDS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/ECT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/ECTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	31	100.0	7	US-09-924-099-4
2	31	100.0	7	US-10-307-276B-40
3	31	100.0	97	US-09-864-408A-5474
4	31	100.0	108	US-09-924-099-1
5	31	100.0	108	US-10-010-729-45
6	31	100.0	108	US-10-307-276B-4
7	31	100.0	108	US-10-307-276B-6
8	31	100.0	108	US-10-803-622-267
9	31	100.0	108	US-10-803-653-267
10	31	100.0	109	US-09-943-906-74
11	31	100.0	109	US-10-435-602-74
12	31	100.0	112	US-10-355-780-1
13	31	100.0	130	US-08-779-784-35

14	31	100.0	130	US-10-010-729-71	Sequence 71, Appl
15	31	100.0	144	US-10-642-120-4	Sequence 4, Appl
16	31	100.0	144	US-10-642-060-4	Sequence 4, Appl
17	31	100.0	144	US-10-642-122-4	Sequence 4, Appl
18	31	100.0	144	US-10-642-124-4	Sequence 4, Appl
19	31	100.0	144	US-10-621-269-4	Sequence 4, Appl
20	31	100.0	144	US-10-620-850-4	Sequence 4, Appl
21	31	100.0	144	US-10-642-116-4	Sequence 4, Appl
22	31	100.0	144	US-10-642-100-4	Sequence 4, Appl
23	31	100.0	144	US-10-642-058-4	Sequence 4, Appl
24	31	100.0	147	US-10-642-121-4	Sequence 4, Appl
25	31	100.0	147	US-10-106-698-6340	Sequence 6340, Ap
26	31	100.0	234	US-10-369-493-9621	Sequence 9621, Ap
27	31	100.0	236	US-10-879-994-6	Sequence 6, Appl
28	31	100.0	237	US-09-924-099-9	Sequence 9, Appl
29	31	100.0	243	US-09-924-099-10	Sequence 10, Appl
30	31	100.0	243	US-09-887-853-6	Sequence 6, Appl
31	31	100.0	243	US-10-683-547-6	Sequence 10, Appl
32	31	100.0	252	US-10-239-656-55	Sequence 55, Appl
33	31	100.0	257	US-10-239-656-67	Sequence 67, Appl
34	31	100.0	267	US-09-766-543-10	Sequence 10, Appl
35	31	100.0	276	US-09-766-543-12	Sequence 12, Appl
36	31	100.0	476	US-10-369-493-19774	Sequence 19774, A
37	31	100.0	483	US-10-369-493-10092	Sequence 10092, A
38	31	100.0	499	US-10-239-656-73	Sequence 73, Appl
39	31	100.0	510	US-10-369-493-19611	Sequence 19611, A
40	31	100.0	566	US-10-369-493-4440	Sequence 4440, Ap
41	31	100.0	567	US-10-369-493-7199	Sequence 7199, Ap
42	31	100.0	574	US-10-369-493-14607	Sequence 14607, A
43	31	100.0	575	US-10-369-493-14397	Sequence 14397, A
44	31	100.0	577	US-10-369-493-10270	Sequence 10270, A
45	31	100.0	583	US-10-369-493-11412	Sequence 11412, A

#### ALIGNMENTS

RESULT 1  
US-09-924-099-4  
; Sequence 4, Application US/09924099  
; Patent No. US20020128450A1  
; GENERAL INFORMATION:  
; APPLICANT: NISHIDA, Yoshihiro  
; APPLICANT: OKURA, Takanori  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: PEPTIDE  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/924, 099  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338, 511  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289, 044/98  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365, 023/98  
; NUMBER OF SEQ ID NOS: 33  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-924-099-4  
Query Match 100.0%; Score 31; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
Db 1 ATSSIDS 7  
RESULT 2

US-10-307-276B-40  
; Sequence 40, Application US/10307276B  
; Publication No. US20040101904A1  
; GENERAL INFORMATION:  
; APPLICANT: William M. Pardridge  
; Ruben J. Boado  
; TITLE OF INVENTION: Delivery of Pharmaceutical Agents  
; Via The Human Insulin Receptor  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Shapiro & Dupont LLP  
; STREET: 233 Wilshire Boulevard, Suite 700  
; CITY: Santa Monica  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90067  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 2000  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/307,276B  
; FILING DATE: 27-Nov-2002  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oldenkamp, David J.  
; REGISTRATION NUMBER: 29,421  
; REFERENCE/DOCKET NUMBER: 0180.0038  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (310) 319-5411  
; TELEFAX: (310) 319-5401  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: polypeptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 40  
US-10-307-276B-40

Query Match 100.0%; Score 31; DB 16; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
Db 1 ATSSIDS 7

RESULT 3  
US-09-864-408A-5474  
; Sequence 5474, Application US/09864408A  
; Publication No. US20040009474A1  
; GENERAL INFORMATION:  
; APPLICANT: Leach, Martin D.  
; APPLICANT: Shimkets, Richard A.  
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Enco  
; FILE REFERENCE: 21402-012  
; CURRENT APPLICATION NUMBER: US/09/864,408A  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: 60/206,690  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 9068  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5474  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-864-408A-5474

Query Match 100.0%; Score 31; DB 11; Length 97;

Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
Db 52 ATSSIDS 58

RESULT 4  
US-09-924-099-1  
; Sequence 1, Application US/09924099  
; Patent No. US20020128450A1  
; GENERAL INFORMATION:  
; APPLICANT: NISHIDA, Yoshihiro  
; APPLICANT: OKURA, Takamori  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: PEPTIDE  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/924,099  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98  
; NUMBER OF SEQ ID NOS: 33  
; SEQ ID NO 1  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-924-099-1

Query Match 100.0%; Score 31; DB 9; Length 108;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
Db 50 ATSSIDS 56

RESULT 5  
US-10-010-729-45  
; Sequence 45, Application US/10010729  
; Publication No. US20030185827A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodriguez, Moses  
; APPLICANT: Miller, David J.  
; APPLICANT: Pease, Larry R.  
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and  
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous  
; FILE REFERENCE: 1199-1-005CIP2  
; CURRENT APPLICATION NUMBER: US/10/010,729  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: 09/730,473  
; PRIOR FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: 09/580,787  
; PRIOR FILING DATE: 2000-05-30  
; PRIOR APPLICATION NUMBER: 09/322,862  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 08/779,784  
; PRIOR FILING DATE: 1997-01-07  
; PRIOR APPLICATION NUMBER: 08/692,084  
; PRIOR FILING DATE: 1996-08-08  
; PRIOR APPLICATION NUMBER: 08/236,520  
; PRIOR FILING DATE: 1994-04-29  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 108

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; TYPE: PRt
; ORGANISM: Mus musculus
US-10-010-729-45
Query Match      100.0%; Score 31; DB 14; Length 103;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATSSIDS 7
        |||||
Db       50 ATSSIDS 56

RESULT 6
US-10-307-276B-4
; Sequence 4, Application US/10307276B
; Publication No. US20040101904A1
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; Ruben J. Boado
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor
;
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapiro & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/307,276B
; FILING DATE: 27-Nov-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-10-307-276B-4

Query Match      100.0%; Score 31; DB 16; Length 108;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATSSIDS 7
        |||||
Db       50 ATSSIDS 56

RESULT 7
US-10-307-276B-6
; Sequence 6, Application US/10307276B
; Publication No. US20040101904A1
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; Ruben J. Boado
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
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; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapiro & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/307,276B
; FILING DATE: 27-Nov-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6
US-10-307-276B-6

Query Match      100.0%; Score 31; DB 16; Length 108;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATSSIDS 7
        |||||
Db       50 ATSSIDS 56

RESULT 8
US-10-803-622-267
; Sequence 267, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
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PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6  
PRIOR FILING DATE: 1990-11-12  
PRIOR APPLICATION NUMBER: GB 9104744.9  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-08  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: Patent version 3.1  
SEQ ID NO 267  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: light chain from clone M1F  
US-10-803-622-267

Query Match 100.0%; Score 31; DB 16; Length 108;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7  
DB 50 ATSSLDS 56

RESULT 9  
US-10-803-653-267  
Sequence 267, Application US/10803653  
Publication No. US20040157215A1  
GENERAL INFORMATION:  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John  
APPLICANT: Pope, Anthony  
APPLICANT: Johnson, Kevin  
APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Griffiths, Andrew  
APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kasper  
APPLICANT: Marks, James  
APPLICANT: Clackson, Timothy  
APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory  
APPLICANT: Bonert, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
FILE REFERENCE: 13839-00013  
CURRENT APPLICATION NUMBER: US/10/803,653  
CURRENT FILING DATE: 2004-03-18  
PRIOR APPLICATION NUMBER: GB 9015198.6  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6  
PRIOR FILING DATE: 1990-11-12  
PRIOR APPLICATION NUMBER: GB 9104744.9  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-08  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: Patent version 3.1  
SEQ ID NO 267  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: light chain from clone M1F  
US-10-803-622-267

PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: Patent version 3.1  
SEQ ID NO 267  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: light chain from clone M1F  
US-10-803-653-267

Query Match 100.0%; Score 31; DB 16; Length 108;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7  
DB 50 ATSSLDS 56

RESULT 10  
US-09-943-906-74  
Sequence 74, Application US/09943906  
Patent No. US20020150571A1  
GENERAL INFORMATION:  
APPLICANT: Frusiner, Stanley B.  
Williamson, R. Anthony  
Burton, Dennis R.  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PRP  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/943,906  
FILING DATE: 30-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/550,374  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Bozicevic, Karl  
REGISTRATION NUMBER: 28,807  
REFERENCE/DOCKET NUMBER: 06510/059001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-5277  
TELEFAX: 415-854-0875  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 74:  
US-09-943-906-74

Query Match 100.0%; Score 31; DB 9; Length 109;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7  
DB 50 ATSSLDS 56

Db 50 ATSSIDS 56

RESULT 11  
US-10-435-602-74  
; Sequence 74, Application US/10435602  
; Publication No. US2003022833A1  
; GENERAL INFORMATION:  
; APPLICANT: Prusiner, Stanley B.  
; APPLICANT: Williamson, R. Anthony  
; APPLICANT: Burton, Dennis R.  
; TITLE OF INVENTION: Antibodies Specific for Native PrPsc  
; FILE REFERENCE: UCAL059CON3  
; CURRENT APPLICATION NUMBER: US/10/435,602  
; CURRENT FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: 09/943,906  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 09/550,374  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 09/036,579  
; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: 08/713,939  
; PRIOR FILING DATE: 1996-09-13  
; PRIOR APPLICATION NUMBER: 08/528,104  
; PRIOR FILING DATE: 1995-09-14  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 74  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: mouse  
US-10-435-602-74

Query Match 100.0%; Score 31; DB 15; Length 109;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7  
Db 50 ATSSIDS 56

RESULT 12  
US-10-355-780-1  
; Sequence 1, Application US/10355780  
; Publication No. US2003014322A1  
; GENERAL INFORMATION:  
; APPLICANT: Prusiner, Stanley  
; APPLICANT: Safar, Jiri  
; APPLICANT: Williamson, Anthony  
; APPLICANT: Burton, Dennis  
; TITLE OF INVENTION: Antibodies Specific for Ungulate PrP  
; FILE REFERENCE: UCAL-194  
; CURRENT APPLICATION NUMBER: US/10/355,780  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: US/09/627,2188  
; PRIOR FILING DATE: 2000-07-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthesized peptide  
US-10-355-780-1

Query Match 100.0%; Score 31; DB 14; Length 112;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATSSIDS 7  
Db 50 ATSSIDS 56

Db 50 ATSSIDS 56

RESULT 13  
US-08-779-784-35  
; Sequence 35, Application US/08779784  
; Publication No. US20020164325A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodriguez, Moses  
; APPLICANT: Miller, David J.  
; APPLICANT: Asakura, Kunihiko  
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM  
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; STREET: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/779,784  
; FILING DATE: 07-JAN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/692,084  
; FILING DATE: 08-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/236,520  
; FILING DATE: 29-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 130 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Mus musculus  
US-08-779-784-35

Query Match 100.0%; Score 31; DB 8; Length 130;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7  
Db 72 ATSSIDS 78

RESULT 14  
US-10-010-729-71  
; Sequence 71, Application US/10010729  
; Publication No. US20030185827A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodriguez, Moses  
; APPLICANT: Miller, David J.

```

; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; FILE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-71

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Query Match          100.0%; Score 31; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 ATSSIDS 7
      |||||
Db      72 ATSSIDS 78

```

```

RESULT 15
US-10-642-120-4
; Sequence 4, Application US/10642120
; Publication No. US20040131610A1
; GENERAL INFORMATION:
; APPLICANT: Thorpe, Philip E.
; APPLICANT: Soares, M. Melina
; APPLICANT: Ran, Sophia
; TITLE OF INVENTION: Methods for Treating Viral Infections Using Antibodies to
; FILE REFERENCE: 4001.002900
; CURRENT APPLICATION NUMBER: US/10/642,120
; PRIOR APPLICATION NUMBER: US 10/621,269
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-120-4

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Query Match          100.0%; Score 31; DB 16; Length 144;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 ATSSIDS 7
      |||||
Db      72 ATSSIDS 78

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Search completed: April 4, 2005, 16:42:45
Job time : 11.3323 secs

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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:32:36 ; Search time 2.52716 seconds

(without alignments)  
266.512 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_183\_189

Perfect score: 31

Sequence: 1 ATSSLDS 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	88	2	PL0261
2	31	100.0	106	2	PL0260
3	31	100.0	106	2	PL0259
4	31	100.0	130	1	KVMSM4
5	31	100.0	131	2	B97737
6	31	100.0	320	2	A13469
7	31	100.0	548	2	F71732
8	31	100.0	555	2	S63137
9	31	100.0	589	2	D70031
10	31	100.0	589	2	F97735
11	31	100.0	600	2	AD3138
12	31	100.0	600	2	H98149
13	31	100.0	604	2	H95974
14	31	100.0	604	2	S60182
15	31	100.0	1025	2	T18376
16	31	100.0	1419	1	DVZOP
17	28	90.3	327	2	F71800
18	28	90.3	327	2	H64716
19	28	90.3	428	2	T43532
20	28	90.3	534	2	S77239
21	28	90.3	546	2	AG1886
22	28	90.3	571	2	S58356
23	28	90.3	575	2	AH1417
24	28	90.3	575	2	AB1793
25	28	90.3	578	2	AB3739
26	28	90.3	584	2	G86713
27	28	90.3	587	2	AD3122
28	28	90.3	587	2	C98165
29	28	90.3	588	2	A75282

30	28	90.3	607	2	A35391	heA protein - Ana
31	28	90.3	609	2	AD3160	heterocyst differ
32	28	90.3	607	2	G71731	mitochondrial tran
33	28	90.3	610	2	H83243	probable ATP-bind
34	28	90.3	611	2	H82351	probable hemolysin
35	28	90.3	614	2	A64180	probable ATP-bind
36	28	90.3	616	2	A12851	hypothetical prote
37	28	90.3	618	2	B81796	probable ABC trans
38	28	90.3	618	2	AB1218	ABC transporter, A
39	28	90.3	619	2	F82391	ABC transporter, A
40	28	90.3	622	2	AB3311	ABC transporter AT
41	28	90.3	626	2	A13310	ABC transporter AT
42	28	90.3	627	2	AH2851	hypothetical prote
43	28	90.3	633	2	T27215	hypothetical prote
44	28	90.3	633	2	G97628	ATP-binding protei
45	28	90.3	634	2	T48418	ABC transporter-11

#### ALIGNMENTS

```
RESULT 1
PL0261
Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997
C:Accession: PL0261
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0261
A:Molecule type: mRNA
A:Residues: 1-88 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-5/Region: framework 1
F:6-16/Region: complementarity-determining 1
F:17-31/Region: framework 2
F:32-38/Region: complementarity-determining 2
F:39-70/Region: framework 3
F:71-79/Region: complementarity-determining 3
F:80-88/Region: framework 4

Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 32 ATSSLDS 38

RESULT 2
PL0260
Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0260
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
```

F:57-88/Region: framework 3  
F:89-97/Region: complementarity-determining 3  
F:98-106/Region: framework 4

Query Match 100.0%; Score 31; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7  
|||||  
50 ATSSLDS 56

## RESULT 3

Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)

C/Species: Mus musculus (house mouse)  
C/Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
C/Accession: P10259

R:Shlomchik, M.; Maccelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.  
J. Exp. Med. 171, 265-297, 1990

A>Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
A/Reference number: P10231; MUID:90111618; PMID:2104919

A/Accession: P10259  
A/Molecule type: mRNA  
A/Residues: 1-106 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1  
F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1  
F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2  
F:57-88/Region: framework 3

F:89-97/Region: complementarity-determining 3  
F:98-106/Region: framework 4

Query Match 100.0%; Score 31; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7  
|||||  
50 ATSSLDS 56

## RESULT 4

Ig kappa chain precursor V region (MOPC 41) - mouse

N/Contents: Ig kappa chain precursor V region VK41  
C/Species: Mus musculus (house mouse)  
C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
C/Accession: A93211; B93211; A93815; A94239; A01922; A01923

R:Seidman, J.G.; Max, E.E.; Leder, P.  
Nature 280, 370-375, 1979

A>Title: A kappa-immunoglobulin gene is formed by site-specific recombination without fu  
A/Reference number: A93211; MUID:79221900; PMID:111146

A/Accession: A93211  
A/Molecule type: DNA  
A/Residues: 1-130 <PC41>

A/Cross-references: UNIPROT:P01639  
A/Accession: B93211  
A/Molecule type: DNA

A/Residues: 1-117 <RV41>  
A/Cross-references: GB:V00804; GB:J00566; NID:952127; PIDN:CAA24186.1; PID:9575660

A/Note: the sequences were determined from the differentially recombined without fu  
R:Burrell, Y.; Schechter, I.  
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977

A>Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors  
A/Reference number: A93815; MUID:77148916; PMID:403522

A/Accession: A93815  
A/Molecule type: protein  
A/Residues: 1-33 <BUR>

A/Note: Met-3 is apparently used as an alternative initiator in 25% of the chains  
R.Gray, W.R.; Dreyer, W.U.; Hood, L.  
Science 155, 465-467, 1967

A>Title: Mechanism of antibody synthesis: size differences between mouse kappa chains.  
A/Reference number: A94239; MUID:67056897; PMID:4162931

A/Accession: A94239  
A/Molecule type: protein  
A/Residues: 23-49, 'B', '51-53, 'LSB', '57-58, 'ZZ', '61-62, 'BZ', '65-76, 'B', '78-108, 110-130 <GRA>

A/Experimental source: Bence Jones protein MOPC 41  
C/Genetics:

A/Introns: 19/1  
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IGA and IGB, the subunits associate into lat  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: alternative initiators; heterotetramer; immunoglobulin  
F:1-22/Domain: signal sequence #status experimental <SIG1>

F:23-130/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>  
F:38-112/Domain: immunoglobulin homology <IMM>

F:45-110/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 130;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7  
|||||  
72 ATSSLDS 78

## RESULT 5

hypothetical protein RC0301 [imported] - Rickettsia conorii (strain Malish 7)

C/Species: Rickettsia conorii  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro

Science 293, 2093-2098, 2001  
A>Title: Mechanisms of evolution in Rickettsia conorii and Rickettsia prowazekii.  
A/Reference number: A97700; MUID:21442074; PMID:11557893

A/Accession: E97737  
A/Status: preliminary  
A/Molecule type: DNA

A/Cross-references: UNIPROT:Q921W9; GB:AE006914; PIDN:AAL02839.1; PID:gl5619360; GSPDB:GT  
C:Superfamily: multidrug resistance protein; ATP-binding cassette homology

A/Residues: 1-131 <KUR>  
A/Cross-references: UNIPROT:Q921W9; GB:AE006914; PIDN:AAL02839.1; PID:gl5619360; GSPDB:GT

A/Accession: E97737  
A/Status: preliminary  
A/Molecule type: DNA

A/Cross-references: UNIPROT:Q921W9; GB:AE006914; PIDN:AAL02839.1; PID:gl5619360; GSPDB:GT  
C:Superfamily: multidrug resistance protein; ATP-binding cassette homology

Query Match 100.0%; Score 31; DB 2; Length 131;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7  
|||||  
62 ATSSLDS 68

## RESULT 6

ABC transporter ATP-binding protein BME11743 [imported] - Brucella melitensis (strain 16b

C/Species: Brucella melitensis  
C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C/Accession: A13469

R:DelVecchio, V.G.; Kaparat, R.U.; Petre, G.; Mujer, C.; Loe, T.; Ivanova, I.  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A/Reference number: AD3252; PMID:11756688

A/Accession: A13469  
A/Status: preliminary  
A/Molecule type: DNA

A/Accession: A13469  
A/Status: preliminary  
A/Molecule type: DNA

A/Accession: A13469  
A/Status: preliminary  
A/Molecule type: DNA

A/Accession: A13469  
A/Status: preliminary  
A/Molecule type: DNA

A/Accession: A13469  
A/Status: preliminary  
A/Molecule type: DNA

A/Cross-references: UNIPROT:Q8YEX4; GB:AE008917; PIDD:AA152924.1; PID:gl1983771; GSPDB:C  
A/Experimental source: strain 16M  
C/Genetics:  
A/Gene: BME11743  
A/Map position: 1

Query Match 100.0%; Score 31; DB 2; Length 320;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7  
|||||  
Db 235 ATSSLDS 241

RESULT 7  
ABC transporter ATP-binding protein (abcT3) RP214 - Rickettsia prowazekii  
C/Species: Rickettsia prowazekii  
C/Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 16-Aug-2004  
A/Cross-references: F71732  
R/Anderson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alsmark, U.  
Nature 396, 133-140, 1998  
A/Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
A/Reference number: A71630; MUID:99039499; PMID:9823893  
A/Accession: F71732  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-548 <AND>  
A/Cross-references: UNIPROT:Q9ZDV5; GB:AJ235270; GB:AJ235269; NID:G3860572; PIDD:CAA1467  
A/Experimental source: strain Madrid E  
C/Genetics:  
A/Gene: abcT3; RP214  
C/Superfamily: ATP-binding cassette homology  
C/Keywords: ATP  
P.323-517/Domain: ATP-binding cassette homology <ABC>

Query Match 100.0%; Score 31; DB 2; Length 548;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7  
|||||  
Db 470 ATSSLDS 476

RESULT 8  
S63137  
hypothetical protein YNL182c - yeast (Saccharomyces cerevisiae)  
M/Alternate names: hypothetical protein N1636  
C/Species: Saccharomyces cerevisiae  
C/Date: 27-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 09-Jul-2004  
A/Accession: S63137  
R/Obermayer, B.; Piravandi, E.; Rinke, M.; Domdey, H.  
submitted to the Protein Sequence Database, April 1996  
A/Reference number: S63122  
A/Accession: S63137  
A/Molecule type: DNA  
A/Residues: 1-555 <OBE>  
A/Cross-references: UNIPROT:P53877; EMBL:Z71458; NID:G1302165; PID:e239555; PID:gl1302166  
A/Experimental source: strain S286C  
C/Genetics:  
A/Gene: MIPS:YNL182c  
A/Cross-references: SGD:S0005126  
A/Map position: 14L

Query Match 100.0%; Score 31; DB 2; Length 555;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7  
|||||  
Db 506 ATSSLDS 512

RESULT 9  
D70031  
ABC transporter (ATP-binding protein) homolog yvnc - Bacillus subtilis  
C/Species: Bacillus subtilis  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
A/Accession: D70031  
R/Kumec, F.; Ogatawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc  
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, C.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gallier  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulo, M.F.;  
Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maeda, S.; Maueel,  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,  
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot,  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.  
A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A/Reference number: A69580; MUID:98044033; PMID:9384377  
A/Accession: D70031  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-589 <KUN>  
A/Cross-references: UNIPROT:Q06967; GB:Z99121; GB:AL009126; NID:G2635827; PIDD:CAB15487.J  
A/Experimental source: strain 168  
C/Genetics:  
A/Gene: yvnc  
C/Superfamily: Escherichia coli ABC transporter mdla; ATP-binding cassette homology  
C/Keywords: ATP; nucleotide binding; P-loop  
P.357-552/Domain: ATP-binding cassette homology <ABC>  
P.374-381/Region: nucleotide-binding motif A (P-loop)

Query Match 100.0%; Score 31; DB 2; Length 589;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7  
|||||  
Db 505 ATSSLDS 511

RESULT 10  
F97735  
hypothetical protein abcT3 [imported] - Rickettsia conorii (strain Malish 7)  
C/Species: Rickettsia conorii  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 16-Aug-2004  
A/Accession: F97735  
R/Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro  
science 293, 2093-2098, 2001  
A/Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A/Reference number: A97700; MUID:21442074; PMID:11557893  
A/Accession: F97735  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-589 <KUR>  
A/Cross-references: UNIPROT:Q921Y4; GB:AE006914; PIDD:AA102824.1; PID:gl5619343; GSPDB:G  
C/Genetics:  
A/Gene: abcT3  
C/Superfamily: ATP-binding cassette homology

Query Match 100.0%; Score 31; DB 2; Length 589;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7  
|||||  
Db 511 ATSSLDS 517

RESULT 11  
AD3138  
hypothetical protein exsA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C:Accession: AD3138  
R:Wood, D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
erige, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB25777, MUID:21608550; PMID:11743193  
A:Accession: AD3138  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-600 <KUR>  
A:Cross-references: UNIPROT:Q8U6S8; GB:AB008689; PIDN:AL45522.1; PID:G17743233; GSPDB:C  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: exsA  
A:Map position: linear chromosome  
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 100.0%; Score 31; DB 2; Length 600;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
|||||  
Db 517 ATSSIDS 523

RESULT 12  
H98149  
ATP-binding transport protein exsA [imported] - Agrobacterium tumefaciens (strain C58, C  
C:Species: Agrobacterium tumefaciens  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 16-Aug-2004  
C:Accession: H98149  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: H98149  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-600 <KUR>  
A:Cross-references: UNIPROT:Q8U6S8; GB:AB007870; PIDN:AAK89722.1; PID:G15158459; GSPDB:C  
C:Genetics:  
A:Gene: AGR\_L\_309  
A:Map position: linear chromosome

Query Match 100.0%; Score 31; DB 2; Length 600;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
|||||  
Db 517 ATSSIDS 523

RESULT 13  
H95974  
mepA-like saccharide exporting ABC transporter protein, consisting of ATP-binding and pe  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 16-Aug-2004  
C:Accession: H95974  
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N<sub>2</sub>-fixing endo

A:Reference number: A95842; MUID:21396508; PMID:11481431  
A:Accession: H95974  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-604 <KUR>  
A:Cross-references: UNIPROT:O52924; GB:AL591985; PIDN:CAC49464.1; PID:G15140950; GSPDB:G  
A:Experimental source: strain 1021, megaplasmid pSymB  
R:Galbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
peta, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
heault, P.; Vandebol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: exsA; SMD20941  
A:genome: plasmid

Query Match 100.0%; Score 31; DB 2; Length 604;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
|||||  
Db 518 ATSSIDS 524

RESULT 14  
S60182  
ATP-binding transport protein exsA - Rhizobium meliloti  
C:Species: Rhizobium meliloti  
C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 16-Aug-2004  
C:Accession: S60182  
R:Becker, A.; Kuester, H.; Niehaus, K.; Puhler, A.  
Mol. Gen. Genet. 249, 487-497, 1995  
A:Title: Extension of the Rhizobium meliloti succinoglycan biosynthesis gene cluster: id  
regulator of succinoglycan biosynthesis.  
A:Reference number: S60181; MUID:96133689; PMID:8544814  
A:Accession: S60182  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-604 <BEC>  
A:Cross-references: UNIPROT:O52924; EMBL:Z50189; NID:G1143532; PIDN:CAA90568.1; PID:G1914  
A:Note: it is uncertain whether Met-1 (ATG), Val-29 (GTG) or Met-74 (ATG) is the initiat  
C:Genetics:  
A:Gene: exsA  
A:Superfamily: ATP-binding cassette homology  
C:Keywords: ATP; nucleotide binding; P-loop  
F:571-565/Domain: ATP-binding cassette homology <ABC>  
F:388-395/Region: nucleotide-binding motif A (P-loop)

Query Match 100.0%; Score 31; DB 2; Length 604;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7  
|||||  
Db 518 ATSSIDS 524

RESULT 15  
T18376  
multidrug resistance protein 2 - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T18376  
R:Kubio, J.P.; Cowman, A.F.  
Exp. Parasitol. 79, 137-147, 1994  
A:Title: Plasmodium falciparum: the pfmdr2 protein is not overexpressed in chloroquine-re  
A:Reference number: Z18924; MUID:94333528; PMID:7914495  
A:Accession: T18376

A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1025 <RUB>  
 A:Cross-references: UNIPROT:Q25693; EMBL:U04640; NID:G439853; FID:G439854; PIDN:AAA21513  
 C/Genetics:  
 A/Gene: mdr2

Query Match 100.0%; Score 31; DB 2; Length 1025;  
 Best Local Similarity 100.0%; Pred. NO. 29;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7  
 |||||  
 Db 851 ATSSIDS 857

Search completed: April 4, 2005, 15:58:02  
 Job time : 3.52716 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 11.8307 seconds  
(without alignments)  
302.988 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_183\_189  
Perfect score: 31  
Sequence: 1 ATSSIDS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03: \*  
1: uniprot\_aprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	57	2 Q7PB38	Q7PB38 rickettsia
2	31	100.0	130	1 KUSG_MOUSE	P01639 mus muscula
3	31	100.0	131	2 Q921W9	Q921W9 rickettsia
4	31	100.0	320	2 Q8YEX4	Q8YEX4 bruceella me
5	31	100.0	370	2 Q61009	Q61009 bacillus an
6	31	100.0	538	2 Q81EL4	Q81EL4 bacillus ce
7	31	100.0	548	2 Q9ZDV5	Q9ZDV5 rickettsia
8	31	100.0	555	1 YNS2_YEAST	P53877 saccharomyc
9	31	100.0	565	2 Q6KFO6	Q6KFO6 chlamydia p
10	31	100.0	565	2 Q9MBU6	Q9MBU6 chlamydia p
11	31	100.0	586	2 Q63CK1	Q63CK1 bacillus ce
12	31	100.0	586	2 Q739U8	Q739U8 bacillus ce
13	31	100.0	586	2 Q6HK05	Q6HK05 bacillus th
14	31	100.0	589	2 Q7PB25	Q7PB25 rickettsia
15	31	100.0	589	2 Q06967	Q06967 bacillus su
16	31	100.0	589	2 Q921Y4	Q921Y4 rickettsia
17	31	100.0	589	2 Q68XP5	Q68XP5 rickettsia
18	31	100.0	596	2 Q9L7X7	Q9L7X7 bruceella ab
19	31	100.0	596	2 Q8RIT1	Q8RIT1 shewanella
20	31	100.0	600	2 Q7NBB3	Q7NBB3 mycoplasma
21	31	100.0	600	2 Q8U6S8	Q8U6S8 agrobacteri
22	31	100.0	601	2 Q98LY9	Q98LY9 rhizobium l
23	31	100.0	602	2 Q82S99	Q82S99 nitrosomon
24	31	100.0	604	2 Q6WZG9	Q6WZG9 rhizobium s
25	31	100.0	604	2 Q52924	Q52924 rhizobium m
26	31	100.0	605	2 Q72QD0	Q72QD0 leprospira
27	31	100.0	605	2 Q8F5R7	Q8F5R7 leprospira
28	31	100.0	606	2 Q7KVA9	Q7KVA9 drosophila
29	31	100.0	610	2 Q7VZM6	Q7VZM6 drosophila
30	31	100.0	616	2 Q7W8H5	Q7W8H5 bordetella
31	31	100.0	616	2 Q7WM37	Q7WM37 bordetella

32	31	100.0	625	2 Q89FS9	Q89FS9 bradyrhizob
33	31	100.0	626	2 Q6CS09	Q6CS09 oikopleura
34	31	100.0	631	2 Q98AT0	Q98AT0 rhizobium 1
35	31	100.0	643	2 Q8XJ66	Q8XJ66 rhizobium 1
36	31	100.0	669	2 Q62E22	Q62E22 burkholderi
37	31	100.0	669	2 Q63J56	Q63J56 burkholderi
38	31	100.0	694	1 ABC7_MOUSE	061102 mus musculu
39	31	100.0	709	2 Q7KVB1	Q7KVB1 drosophila
40	31	100.0	715	2 Q8KRA4	Q8KRA4 rhizobium e
41	31	100.0	743	2 Q9W0C5	Q9W0C5 drosophila
42	31	100.0	752	1 ABC7_HUMAN	Q75027 homo sapien
43	31	100.0	752	2 Q7O4E8	Q7O4E8 rattus norv
44	31	100.0	888	2 Q7RBT4	Q7RBT4 plasmodium
45	31	100.0	947	2 Q08667	Q08667 plasmodium

## ALIGNMENTS

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RESULT 1
Q7PB38 PRELIMINARY; PRT; 57 AA.
ID Q7PB38;
AC Q7PB38;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding protein.
GN Name=trsb_0rf.406;
OS Rickettsia sibirica.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=35793;
RN [1]
RP SEQUENCE FROM N.A.
RA Malek J.A., Ereemeva M.E., Dasch G.A.;
RL Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.
CC -! SIMILARITY: Belongs to the ABC transporter family.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABW01000001; EAA25646.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR Prodom; PD000006; ABC transporter; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
KW ATP-binding.
SQ
SEQUENCE 57 AA; 6232 MW; 4FA4E36794DE92B8 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7
Db 48 ATSSIDS 54

RESULT 2
KV5G_MOUSE STANDARD; PRT; 130 AA.
ID KV5G_MOUSE;
AC P01639; P01640;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region MOPC 41 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=79221900; PubMed=111146;
RA Seidman J.G., Max E.E., Leder P.,
RT "A kappa-immunoglobulin gene is formed by site-specific recombination
RT without further somatic mutation.";
RL Nature 280:370-375 (1979).
RN [2]
RP SEQUENCE OF 1-33.
RX MEDLINE=77148916; PubMed=403522;
RA Buretein Y., Schechter I.;
RT "Amino acid sequence of the NH2-terminal extra piece segments of the
RT precursors of mouse immunoglobulin lambda1-type and kappa-type light
RT chains";
RL Proc. Natl. Acad. Sci. U.S.A. 74:716-720 (1977).
RN [3]
RP SEQUENCE OF 23-130.
RX MEDLINE=67056897; PubMed=4162931;
RA Gray W.R., Dreyer W.J., Hood L.;
RT "Mechanism of antibody synthesis: size differences between mouse kappa
RT chains";
RL Science 155:465-467 (1967).
CC -1- MISCELLANEOUS: This precursor was synthesized in a cell-free
CC system directed by mRNA isolated from myeloma polyomes.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR HSSP; A93211; KVM5M4.
DR HSSP; P01594; IJVS.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 130 Ig kappa chain V-V region MOPC 41.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 119 Complementarity-determining-3.
FT DOMAIN 120 129 Framework-4.
FT DISULFID 45 110 By similarity.
FT VARIANT 1 2 Missing (in 25% of the molecules).
FT NON TER 130 130
SQ SEQUENCE 130 AA; 14311 MW; SEFDFE71D5F1BEC CRC64;

Query Match 100.0%; Score 31; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
DB 72 ATSSIDS 78

RESULT 3
Q921W9 PRELIMINARY; PRT; 131 AA.
AC Q921W9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding protein.
GN Ordered locus names=RC0301;
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893; DOI=10.1126/science.1061471;

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RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Sameon D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098 (2001).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE008596; AA02839.1; -.
DR PIR; E97737; E97737.
DR HSSP; P08716; 1MT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR Prodom; PD000006; ABC_transporter; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 131 AA; 14753 MW; C8484BCA612872D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
DB 62 ATSSIDS 68

RESULT 4
Q8YEY4 PRELIMINARY; PRT; 320 AA.
AC Q8YEY4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC TRANSPORTER ATP-BINDING PROTEIN.
GN Ordered locus names=BME11743;
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756588; DOI=10.1073/pnas.221575398;
RA Delvecchio V.G., Kapatal V., Redkar R.J., Patia G., Mujar C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykdis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman B.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriades N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE009607; AA152924.1; -.
DR PIR; A13469; A13469.
DR HSSP; Q9KQW9; 1PP4.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR Pfam; PF00005; ABC_tran; 1.
DR Prodom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 320 AA; 35768 MW; 95DBAB38430A2C01 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 320;
Best Local Similarity 100.0%; Pred. No. 50;

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSIDS 7
Db 235 ATSSIDS 241

RESULT 5
061009 PRELIMINARY; PRT; 370 AA.
AC 061009;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE ABC transporter.
GN OrderedLocusNames=BA51815;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Stearne;
RA Bretin T.S., Bruce D., Challacombe J.F., Gina P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin B., Tice H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE017225; AAT54130.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane_1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding.
SQ
SEQUENCE 370 AA; 40954 MW; 9C6683290C2C7EC3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 370;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSIDS 7
Db 290 ATSSIDS 296

RESULT 6
081E14 PRELIMINARY; PRT; 538 AA.
AC 081E14;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding and permease
DE protein.
GN OrderedLocusNames=BC1955;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,

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RA Kapral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goldsman E., Larsen N., D'Souza M., Malinas T.,
RA Grechkin Y., Busch G., Haselkorn R., Fontein M., Ehrlich S.D.,
RA Overbeek R., Kyprides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
CC -1 SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE017004; AAP08926.1; -.
DR HSSP; Q9CHL8; 1MV5.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane_1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ
SEQUENCE 538 AA; 59151 MW; B70E78C62BEAC132 CRC64;

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 538;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSIDS 7
Db 458 ATSSIDS 464

RESULT 7
092DV5 PRELIMINARY; PRT; 548 AA.
AC 092DV5;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE ABC TRANSPORTER ATP-BINDING PROTEIN (AbcT3).
GN OrderedLocusNames=RP214;
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxId=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893; DOI=10.1038/24094;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Scheritz-Ponten T., Aleksei U.C.M., Podewski R.M., Neeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
CC -1 SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AJ235270; CAA14677.1; -.
DR PIR; F71732; F71732.
DR HSSP; P08716; 1MT0.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.

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DR InterPro; IPR003439; ABC\_transporter.  
 DR Pfam; PF00664; ABC\_membrane; 1.  
 DR Pfam; PF00005; ABC\_tran; 1.  
 DR ProDom; PD000006; ABC\_transporter; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR PROSITE; PS00929; ABC\_TM1F; 1.  
 DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
 DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 1.  
 KW ATP-binding; Complete proteome.  
 SQ SEQUENCE 548 AA; 62589 MW; B4ED4E7F9D53EDC9 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 548;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7  
 Db 470 ATSSLDS 476

RESULT 8  
 ID YNS2 YEAST STANDARD; PRT; 555 AA.  
 AC P53877;  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Hypoetical 61.8 kDa Trp-Asp repeats containing protein in NPRI-RPS3  
 GN Intergenic region.  
 OS OrderedLocustNames=YNL182C; ORFNames=N1636;  
 OS Saccharomyces cerevisiae (Baker's Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Obermaier B., Piravandi E., Rinke M., Domdey H.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 4 WD repeats.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; Z71458; CAA96075.1; -.  
 DR PIR; S63137; S63137.  
 DR IntAct; P53877; -.  
 DR GeneOnline; 143188; -.  
 DR SGD; S00005126; IPI3.  
 DR GO; GO:0005634; C:nucleus; IDA.  
 DR InterPro; IPR001680; WD40.  
 DR InterPro; IPR011045; WD40\_like.  
 DR Pfam; PF00400; WD40; 2.  
 DR SMART; SM00320; WD40; 3.  
 DR PROSITE; PS00678; WD\_REPEATS\_1; FALSE\_NEG.  
 DR PROSITE; PS50082; WD\_REPEATS\_2; 1.  
 DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
 KW Hypoetical protein; Repeat; WD repeat.  
 FT REPEAT 90 133 WD 1.  
 FT REPEAT 137 176 WD 2.  
 FT REPEAT 187 234 WD 3.  
 FT REPEAT 342 383 WD 4.  
 SQ SEQUENCE 555 AA; 61773 MW; 8EED6854DF9405A6 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

Db 506 ATSSLDS 512

RESULT 9  
 ID Q6KF06 PRELIMINARY; PRT; 565 AA.  
 AC Q6KF06;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Structural protein.  
 OS Chlamydia phage 3.  
 OC Viruses; ssDNA viruses; Microviridae; Chlamydiaviruses.  
 OX NCBI\_TaxID=225067;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Garner S.A., Everson J.S., Lambden P.R., Fane B.A., Clarke I.N.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ550635; CAD79477.1; -.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR003514; Capsid\_F.  
 DR Pfam; PF02305; Phage\_F; 1.  
 SQ SEQUENCE 565 AA; 63629 MW; E8DEBAE70FA91DFE CRC64;

Query Match 100.0%; Score 31; DB 2; Length 565;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7  
 Db 497 ATSSLDS 503

RESULT 10  
 ID Q9MBU6 PRELIMINARY; PRT; 565 AA.  
 AC Q9MBU6;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Structural protein.  
 GN Name=VPI;  
 OS Chlamydia phage 2.  
 OC Viruses; ssDNA viruses; Microviridae; Chlamydiaviruses.  
 OX NCBI\_TaxID=105154;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20193783; PubMed=10729119;  
 RX DOI=10.1126/JVI.74.8.3464-3469.2000;  
 RA Liu B., Everson J.S., Fane B., Giannikopoulos P., Vreton E.,  
 RA Lambden P.R., Clarke I.N.;  
 RT "Molecular characterisation of a bacteriophage (Chp2) from Chlamydia  
 RT peitraci.";  
 RL J. Virol. 74:3464-3469(2000).  
 DR EMBL; AJ270057; CAB85589.1; -.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR003514; Capsid\_F.  
 DR Pfam; PF02305; Phage\_F; 1.  
 SQ SEQUENCE 565 AA; 63538 MW; 670485CDCA94932 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 565;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7  
 Db 497 ATSSLDS 503

RESULT 11

```
063CK1
ID 063CK1 PRELIMINARY; PRT; 586 AA.
AC 063CK1;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Multidrug ABC transporter, ATP-binding protein.
GN ORFName=BRX1771;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=288681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZK;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18482.1; -.
KW ATP-binding.
SQ
SEQUENCE 586 AA; 64902 MW; BCE45D1F31C7CE7B CRC64;
OX
NCBI_TaxId=180856;

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 586;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 506 ATSSLDS 512

RESULT 12
ID 0739U8 PRELIMINARY; PRT; 586 AA.
AC 0739U8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE ABC transporter, ATP-binding/permease protein.
GN OrderedLocNames=BCE2040;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=222523;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed14960714; DOI=10.1093/nar/gkh258;
RA Raeko D.A., Ravel J., Oekstad O.A., Helgason E., Car R.Z., Yang L.,
RA Shores K.A., Foua D.E., Tourasse N.J., Angluoli S.V., Kolczay J.F.,
RA Nelson W.C., Kolstoe A.B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
CC -1 SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE017270; AAS40963.1; -.
DR TIGR; BCE2040; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR011440; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
```

```
SQ SEQUENCE 586 AA; 64869 MW; AA81400A8BA84193 CRC64;
OX
NCBI_TaxId=180856;

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 586;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 506 ATSSLDS 512

RESULT 13
ID 06HK05 PRELIMINARY; PRT; 586 AA.
AC 06HK05;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Multidrug resistance ABC transporter, ATP-binding and permease.
GN OrderedLocNames=BR9727_1789;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=180856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AB017355; AAT59651.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR011440; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 586 AA; 64916 MW; 662AA920E116F5C4 CRC64;
OX
NCBI_TaxId=180856;

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 586;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 506 ATSSLDS 512

RESULT 14
ID 07PB25 PRELIMINARY; PRT; 589 AA.
AC 07PB25;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding protein.
GN Name=rib Of.420;
OS Rickettsia sibirica.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
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OX NCB1_TaxID=35793;
RN [1]
RP SEQUENCE FROM N.A.
RA Malek J.A., Ereemeva M.E., Dasch G.A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AB001000001; EAA25659.1; -.
DR HSSP; O9CHL8; 1MW5.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR011527; ABC membrane 1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR Prodom; PD000006; ABC_transporter; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS0893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; 589 AA; 67091 MW; 3ELFC057195F20DD CRC64;
SQ SEQUENCE 589 AA; 67091 MW; 3ELFC057195F20DD CRC64;

Query Match 100.0%; Score 31; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 511 ATSSLDS 517

RESULT 15
006967 PRELIMINARY; PRT; 589 AA.
AC 006967; Q795F6;
DT 01-JUN-1997 (TrEMBLrel. 04, Created)
DT 01-JUN-1997 (TrEMBLrel. 04, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein yvcc.
GN Name=yvcc; OrderedLocustNames=BSU34820;
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCB1_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Denisot F.C.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertolo M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boriss R., Boursier L., Brans A., Braun M., Bignelli S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denisot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Ertlan K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holappel S., Hosono S., Hullo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kaashara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Maeda S., Meuel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,

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RA Park S.H., Parro V., Pohl T.M., Portetelle D., Potworilik S.,
RA Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,
RA Ray M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadate Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scottone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takuchi M., Tamakoshi A., Tanaka T., Terpsira P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenhol M., Vannier F.,
RA Vassariotti A., Viart A., Wambut R., Wedler E., Wedler H.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E.,
RA Yoshikawa H., Zanchin A.;
RT "the complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; Z94043; CAB08051.1; -.
DR EMBL; Z99121; CAB15487.1; -.
DR PIR; D70031; D70031.
DR HSSP; O9CHL8; 1MW5.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC membrane 1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR Prodom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS0893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome; Hypothetical protein.
SQ SEQUENCE 589 AA; 64519 MW; 8A15163B5698DA08 CRC64;

```

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Query Match 100.0%; Score 31; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 505 ATSSLDS 511

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Search completed: April 4, 2005, 15:56:14  
 Job time : 17.8307 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:19:49 ; Search time 17.9712 Seconds  
(without alignments)  
193.690 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_222\_230  
Perfect score: 49  
Sequence: 1 LQYAFPYR 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp19808:\*
- 2: geneseqp19908:\*
- 3: geneseqp20008:\*
- 4: geneseqp20018:\*
- 5: geneseqp20028:\*
- 6: geneseqp20038:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	107	3	AAV90824
2	49	100.0	243	2	AAW02280
3	49	100.0	243	2	AAW53170
4	49	100.0	243	2	AAW80424
5	49	100.0	243	7	ABW00716
6	49	100.0	246	2	AAW39569
7	49	100.0	267	4	AAU04944
8	49	100.0	409	4	AAU04945
9	44	89.8	534	2	AAW39571
10	43	87.8	108	8	AD126702
11	41	83.7	107	8	AD25834
12	40	81.6	107	4	AD25833
13	36	73.5	9	4	AAW60407
14	36	73.5	9	4	AAW61592
15	36	73.5	9	5	AAU76520
16	36	73.5	9	5	AAE15818
17	36	73.5	9	8	ADJ78015
18	36	73.5	9	8	ADJ88015
19	36	73.5	9	8	ADN12061
20	36	73.5	9	8	ADP43336
21	36	73.5	9	8	ADJ18660
22	36	73.5	89	2	AAW80080
23	36	73.5	92	2	AAW95477
24	36	73.5	107	4	AAW62083
25	36	73.5	107	4	AAW62085

26	36	73.5	107	4	AAW60398	AAW60398 Humanised
27	36	73.5	107	4	AAW60396	AAW60396 Mouse ant
28	36	73.5	107	4	AAW61583	AAW61583 Humanised
29	36	73.5	107	4	AAW61581	AAW61581 Murine 2C
30	36	73.5	107	5	AAE15812	AAE15812 Human mAb
31	36	73.5	107	6	ABG74718	ABG74718 Murine hu
32	36	73.5	107	6	ABG74702	ABG74702 Murine hu
33	36	73.5	107	7	ABR83149	ABR83149 Murine hu
34	36	73.5	107	7	ABR83149	ABR83149 Hu007 ant
35	36	73.5	107	7	ABR83156	ABR83156 Hu007 ant
36	36	73.5	107	7	ABR83157	ABR83157 Hu007 ant
37	36	73.5	107	7	ABR83157	ABR83157 Humanise
38	36	73.5	107	8	AD271452	AD271452 Murine mo
39	36	73.5	107	8	AD271450	AD271450 Murine mo
40	36	73.5	107	8	ADJ88006	ADJ88006 Humanised
41	36	73.5	107	8	ADN12050	ADN12050 Variable
42	36	73.5	107	8	ADN12052	ADN12052 Variable
43	36	73.5	107	8	ADP43326	ADP43326 Humanised
44	36	73.5	107	8	ADP43324	ADP43324 Humanised
45	36	73.5	107	8	ADR73589	ADR73589 Anti-AR a

## ALIGNMENTS

RESULT 1	AAV90824	standard; protein; 107 AA.
ID	AAV90824	
XX	AAV90824;	
AC	AAV90824;	
XX	AAV90824;	
DT	29-AUG-2000	(first entry)
XX	29-AUG-2000	
DE	520C9 hybridoma VL domain SEQ ID NO:26.	
XX	520C9 hybridoma VL domain SEQ ID NO:26.	
KW	Antigen binding site; immunoglobulin; cancer antigen; immunological;	
KW	antibody; tumour; human; cancer; cytostatic; hybridoma;	
KW	specific binding assay; affinity purification; drug targeting;	
KW	toxin targeting; imaging; genetic; therapeutic.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	Homo sapiens.	
PN	US6054561-A.	
XX	US6054561-A.	
PD	25-APR-2000.	
XX	25-APR-2000.	
PF	07-JUN-1995;	95US-00483749.
XX	07-JUN-1995;	
PR	08-FEB-1984;	84US-00577976.
PR	11-JAN-1985;	85US-00690750.
PR	21-MAR-1986;	86US-00842476.
PR	08-MAY-1986;	88US-00190778.
PR	11-AUG-1994;	94US-00288981.
XX	11-AUG-1994;	
PA	(CHIR ) CHIRON CORP.	
XX	(CHIR ) CHIRON CORP.	
PI	Ring DB;	
XX	Ring DB;	
DR	WPI; 2000-338508/29.	
DR	WPI; 2000-338508/29.	
XX	N-PSDB; AAA38908.	
XX	N-PSDB; AAA38908.	
PT	Monoclonal antibody capable of binding to human breast cancer antigen	
PT	useful for affinity purification, drug or toxin targeting, imaging, and	
XX	treating cancer.	
PS	Disclosure; Fig 13; 57pp; English.	
XX	Disclosure; Fig 13; 57pp; English.	
CC	The present invention describes a monoclonal antibody (Mab) (I) that	
CC	binds to a human breast cancer antigen that is also bound by Mab 454C11	
CC	and 520C9 (produced by hybridoma ATCC HB8484 and HB8696, respectively).	
CC	described is a hybridoma that produces (I). (I) is useful in specific	
CC	binding assays, affinity purification, drug or toxin targeting, imaging,	
CC	and genetic or immunological therapeutics for various cancers. The	

CC Present sequence represents a VL domain derived from a 520C9 hybridoma,  
CC which is used in the exemplification of the present invention  
SQ Sequence 107 AA;

Query Match 100.0%; Score 49; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.057;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYALFPYT 9  
DB 89 LQYALFPYT 97

RESULT 2  
ID AAM02280 standard; protein; 243 AA.

AC AAM02280;

DT 25-MAR-2003 (revised)  
DT 29-OCT-1996 (first entry)

DE 520C9 anti-c-erbB-2 two single chain Fv construct.

XX 520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sfv;  
XX construct; polypeptide linker; C-terminal amino acid sequence;  
XX in vivo imaging; drug targeting experiment; homodimer; increased;  
XX binding avidity; tissue retention time.

OS Homo sapiens.

FH Key Location/Qualifiers  
FT Peptide 118..133  
FT /label= linker

XX US5534254-A.

XX 09-JUL-1996.

XX 07-OCT-1993; 93US-00133804.

XX 06-FEB-1992; 92US-00831967.

XX (CHIR ) CHIRON CORP.  
XX (CREA-) CREATIVE BIOMOLECULES INC.

XX Oppermann H, Ring DB, Huston JS, Houston LL;

XX WPI; 1996-333194/33.

XX DR N-PSDB; AAT36880.

XX Compans. contg. antigen-targeting antibody fragment constructs -  
PT comprising dimer of single-chain Fv fragments.

XX Example 1; Col 33-36; 30pp; English.

XX Variable heavy (VH) and variable light (VL) genes were cloned from a  
XX 520C9 hybridoma CDNA library, using probes directed toward the antibody  
XX constant and joining regions. A two single chain Fv (sfv) gene was  
XX constructed by connecting the VH and VL genes with a Ser rich polypeptide  
XX linker. The resulting 520C9 two sfv gene, which encodes the present  
XX sequence, was inserted into an expression vector, transformed into E.  
XX coli, and protein expression induced by the addn. of IPTG to the culture  
XX medium. A compsn. comprising a carrier and the 2 sfv protein prod. can be  
XX used for in vivo imaging, and drug targeting experiments. The 2 sfv  
XX protein prod. is a homodimer, in which both fragments target the same  
XX antigen, therefore giving greater binding avidity and longer tissue  
XX retention times, compared to individual sfv protein prod. fragments.  
XX (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 243 AA;

Query Match 100.0%; Score 49; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYALFPYT 9  
DB 222 LQYALFPYT 230

RESULT 3  
ID AAM53170 standard; protein; 243 AA.

AC AAM53170;

DT 16-JUL-1998 (first entry)

DE 520C9 anti-c-erbB-2 sfv' dimeric construct protein sequence.

XX Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer; c-erbB-2;  
XX tumour; diagnosis; sg.

OS Synthetic.

OS Mus sp.

XX US5753204-A.

XX 19-MAY-1998.

XX 05-JUN-1995; 95US-00461838.

XX 06-FEB-1992; 92US-00831967.

XX 07-OCT-1993; 93US-00133804.

XX (CHIR ) CHIRON CORP.  
XX (CREA-) CREATIVE BIOMOLECULES INC.

XX Oppermann H, Ring DB, Huston JS, Houston LL;

XX WPI; 1998-311318/27.

XX DR N-PSDB; AAV21798.

XX Imaging of antigens in vivo - using dimers of single-chain antibody Fv  
XX fragments.

XX Example 1; Col 33-36; 30pp; English.

XX This represents the protein sequence of a 520C9 sfv' (single chain Fv)  
XX construct. This was constructed by connecting the VH and VL genes with a  
XX DNA sequence encoding a Serine rich linker. 520C9 is a monoclonal  
XX antibody useful in targeting c-erbB-2 antigen. This dimeric construct can  
XX be used in the methods of invention of imaging a preselected antigen  
XX expressed in a mammal. The methods are used in magnetic resonance imaging  
XX of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic  
XX constructs have enhanced properties as in vivo targeting agents in  
XX comparison with intact monoclonal antibodies or their Fab fragments. The  
XX antigen constructs permit the in vivo targeting of an epitope on an  
XX antigen with greater apparent avidity, including greater tumour  
XX specificity, tumour localisation and tumour retention properties than  
XX that of the Fab fragment having the same CDRs as the construct

XX Sequence 243 AA;

Query Match 100.0%; Score 49; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYALFPYT 9  
DB 222 LQYALFPYT 230

RESULT 4

```

AAW80424
ID AAW80424 standard; protein; 243 AA.
XX
AC AAW80424;
XX
DT 28-JAN-1999 (first entry)
XX
DE 520C9 sFv sequence.
XX
KM 520C9 sFv; antigen; tumour cell; antibody 520C9; targeted delivery;
XX antigen-expressing cell.
XX
OS Synthetic.
XX
PN US5837846-A.
XX
PD 17-NOV-1998.
XX
PF 05-JUN-1995; 95US-00461386.
XX
PR 06-FEB-1992; 92US-00831967.
XX
PR 07-OCT-1993; 93US-00133804.
XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
XX (CHIR ) CHIRON CORP.
XX
PI Oppermann H, Houston LL, Huston JS, Ring DB;
XX
DR WPI; 1999-023541/02.
XX
DR N-PSDB; AAW63399.
XX
PT Nucleic acid encoding single-chain Fv fragment specific for antigens -
PT and having C-terminal tail for crosslinking to form dimer with improved
PT pharmacokinetic properties, used to deliver drugs and imaging agents,
PT especially to tumours.
XX
PS Example 1; Col 35-36; 29pp; English.
XX
CC The present sequence represents an antibody 520C9 sFv. Variable heavy and
CC light sequences of antibody 7520C9 are connected, together with a serine
CC linker, to produce the present single chain Fv gene. The present sequence
CC exemplifies the invention. Dimers of the single chain Fv are used for
CC targeted delivery of drugs or imaging agents (e.g. cytotoxins, produgs
CC or 9m-technetium) to antigen-expressing cells, particularly for
CC treatment or diagnosis of tumours (especially of ovary or breast)
CC
SQ Sequence 243 AA;

Query Match 100.0%; Score 49; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYAFPYT 9
DB 222 LQYAFPYT 230

RESULT 5
ABW00716
ID ABW00716 standard; protein; 243 AA.
XX
AC ABW00716;
XX
DT 15-JAN-2004 (first entry)
XX
DE 520C9 sFv protein.
XX
KM Cell proliferation; cytotoxic agent; drug targeting; single-chain Fv;
XX sFv.
XX
OS Unidentified.
XX
PN US2002168375-A1.

```

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XX
PD 14-NOV-2002.
XX
XX
PF 21-JUN-2001; 2001US-00887853.
XX
XX
PR 06-FEB-1992; 92US-00831967.
XX 07-OCT-1993; 93US-00133804.
PR 05-JUN-1995; 95US-00462641.
XX 26-APR-2000; 2000US-00558741.
XX
PA (CHIR ) CHIRON CORP.
XX
XX
PI Huston JS, Houston LL, Ring DB, Oppermann H;
XX
DR WPI; 2003-765156/72.
XX
DR N-PSDB; AAD61485.
XX
PT Novel binding protein formulation for targeting epitope on antigen in
PT mammal, comprising dimeric biosynthetic construct having conformation
PT permitting binding of antigen by binding site of each polypeptide chain.
XX
XX
PS Example 1; Page 19-20; 30pp; English.
XX
XX
CC The invention relates to a binding protein formulation for targeting an
CC epitope on an antigen expressed in mammal. The formulation comprises of
CC dimeric biosynthetic construct having conformation permitting binding of
CC antigen by binding site of each polypeptide chain. The invention is
CC useful for imaging a preselected antigen in a mammal expressing the
CC antigen. It is also useful for targeting drugs that inhibit cell
CC proliferation and cytotoxic agents that kill cells. The present sequence
CC is 520C9 sFv protein. This sequence is used in the exemplification of the
CC invention
CC
SQ Sequence 243 AA;

Query Match 100.0%; Score 49; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYAFPYT 9
DB 222 LQYAFPYT 230

RESULT 6
AAR39569
ID AAR39569 standard; protein; 246 AA.
XX
AC AAR39569;
XX
DT 25-MAR-2003 (revised)
XX 07-FEB-1994 (first entry)
DT
XX
DE Sequence of 520C9 sFv protein.
XX
XX
KM Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;
XX biosynthetic single polypeptide chain binding site; ss.
XX
OS Synthetic.
XX
PN WO9316185-A2.
XX
XX
PD 19-AUG-1993.
XX
XX
PF 05-FEB-1993; 93WO-US001055.
XX
XX
PR 06-FEB-1992; 92US-00831967.
XX
XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
XX (CETU ) CETUS ONCOLOGY CORP.
XX
PI Huston JS, Houston LL, Ring DB, Oppermann H;
XX

```

DR WPI: 1993-272889/34.  
DR N-PSDB; AAQ46084.  
XX  
PT New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for  
PT imaging or treating breast or ovarian cancer etc.  
XX  
PS Claim 4; Page 60-61; 87pp; English.  
XX  
CC C-erbB-2 refers to a protein antigen expressed on the surface of tumour  
CC cells, such as breast and ovarian tumour cells, which is an approx.  
CC 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about  
CC 5.3 (see AAQ46083, AAR39568). A single chain Fv (scFv) is a covalently  
CC linked VH-VL heterodimer which is expressed from a gene fusion including  
CC VH- and VL- encoding genes connected by a peptide-encoding linker. Such  
CC linker sequences are set forth in AA residues 116-135 in AAR39569, which  
CC includes part of the 16 AA linker sequences in AAR39572. Using AAQ46084  
CC for the 520C9 monoclonal antibody, a single chain polypeptide can be  
CC produced having a binding affinity for a C-erbB-2 related antigen. 'X' in  
CC AAR39569 refers to the location of a stop codon in AAQ46084. (Updated on  
CC 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 246 AA;  
XX  
Query Match 100.0%; Score 49; DB 2; Length 246;  
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Gaps 0;  
Matches 9; Conservative 0; Indels 0; Indels 0; Gaps 0;  
XX  
QY 1 LQYAIFFPT 9  
DB 222 LQYAIFFPT 230  
XX  
RESULT 7  
AAU04944  
ID AAU04944 standard; protein; 267 AA.  
XX  
AC AAU04944;  
XX  
DT 06-AUG-2003 (revised)  
DT 24-OCT-2001 (first entry)  
XX  
XX Humanised anti-p185 single chain antibody; 520C9H.  
XX  
KW Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunoconjugate;  
KM cancer; tumour; adenocarcinoma.  
XX  
XX Homo sapiens.  
OS Mus sp.  
OS Synthetic.  
OS Chimeric.  
XX  
FH Key  
FT 53. .57  
FT Location/Qualifiers  
FT /label= CDR  
FT /note= "Complementarity determining region"  
FT 72. .88  
FT /label= CDR  
FT /note= "Complementarity determining region"  
FT 121. .126  
FT /label= CDR  
FT /note= "Complementarity determining region"  
FT 138. .152  
FT /label= Synthetic peptide linker  
FT /note= "links the heavy chain to the light chain"  
FT 176. .186  
FT /label= CDR  
FT /note= "Complementarity determining region"  
FT 202. .208  
FT /label= CDR  
FT /note= "Complementarity determining region"  
FT 241. .249  
FT /label= CDR  
FT /note= "Complementarity determining region"

FT Region 260. .267  
FT /label= Glu\_Glu\_epitope  
XX  
XX WO200153354-A2.  
XX  
XX 26-UTL-2001.  
XX  
XX 19-JAN-2001; 2001WO-US001919.  
XX  
XX 20-JAN-2000; 2000US-0177258P.  
XX  
XX (CHTR ) CHIRON CORP.  
XX (HAMT-) HAMILTON CIVIC HOSPITALS RES DEV INC.  
XX (HAMT-) HAMILTON REGIONAL CANCER CENT.  
XX  
XX Austin R, Kwok CS, Ring DB;  
XX  
XX WPI: 2001-451904/48.  
XX N-PSDB; AAS09507.  
XX  
XX Novel immunoconjugate useful for inhibiting tumor cell growth in vivo  
XX comprises a humanized anti-p185 antibody linked to an Interleukin-2  
XX polypeptide.  
XX  
XX Claim 7; Fig 9; 74pp; English.  
XX  
XX The sequence represents a humanised anti-p185 single chain antibody which  
XX is linked to a human interleukin-2 (IL-2) molecule to make a fusion  
XX protein. The fusion protein (or immunoconjugate) is used to inhibit the  
XX growth of tumours or cancers particularly those characterised by  
XX overexpression of p185 e.g. human adenocarcinomas and malignant and/or  
XX benign tumours of the breast, renal system, salivary gland,  
XX gastrointestinal tract or gastric tumours. (Updated on 06-AUG-2003 to  
XX correct OS field.)  
XX  
SQ Sequence 267 AA;  
XX  
Query Match 100.0%; Score 49; DB 4; Length 267;  
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Gaps 0;  
Matches 9; Conservative 0; Indels 0; Indels 0; Gaps 0;  
XX  
QY 1 LQYAIFFPT 9  
DB 241 LQYAIFFPT 249  
XX  
RESULT 8  
AAU04945  
ID AAU04945 standard; protein; 409 AA.  
XX  
AC AAU04945;  
XX  
DT 06-AUG-2003 (revised)  
DT 24-OCT-2001 (first entry)  
XX  
XX Humanised anti-p185 antibody/IL-2 fusion protein.  
XX  
KW Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunoconjugate;  
KM cancer; tumour; adenocarcinoma; fusion protein.  
XX  
XX Homo sapiens.  
OS Mus sp.  
OS Synthetic.  
OS Chimeric.  
XX  
FH Key  
FT 1. .22  
FT Location/Qualifiers  
FT /label= Signal\_peptide  
FT 23. .409  
FT /label= Mature\_fusion\_protein  
FT 23. .259  
FT /label= Humanised\_antibody\_520C9H  
FT 53. .57  
FT Region



Qy	Db	Query Match	Best Local Similarity	Score 49;	DB 4;	Length 409;	Matches 9;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1	1QYAIFPYT	9		100.0%	Pred. No. 0.23;		241	1QYAIFPYT	249		
RESULT 9											

ID	AA039571	standard; protein; 534 AA.
AC	AA039571;	
XX		
XX		
DT	25-MAR-2003 (revised)	
DT	07-FEB-1994 (first entry)	
XX		
DE	Sequence of G-FIT.	
XX		
XX	Tumour antigen; c-erbB-2; G-FIT.	
OS	Synthetic.	
XX		
PN	W09316185-A2.	
XX		
PD	19-AUG-1993.	
XX		
XX		
PF	05-FEB-1993; 93WO-US001055.	
XX		
PR	06-FEB-1992; 92US-00831967.	
XX		
XX	(CREA-) CREATIVE BIOMOLECULES INC.	
PA	(CETU) CETUS ONCOLOGY CORP.	
XX		
PI	Hueton JS, Hueton LL, Ring DB, Oppermann H;	
XX		
DR	WPI; 1993-272889/34.	
DR	N-PSDB; AA046086.	
XX		
PT	New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for	
PT	imaging or treating breast or ovarian cancer etc.	
XX		
PS	Example; Page 65-68; 87pp; English.	
XX		
CC	c-erbB-2 refers to a protein antigen expressed on the surface of tumour	
CC	cells. Such as breast and ovarian tumour cells, which is an approx.	
CC	200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about	
CC	5.3 (see AA046083, AA039568). (Updated on 25-MAR-2003 to correct PN	
CC	field.)	
XX		
XX		
SQ	Sequence 534 AA;	
Query Match	89.8%;	Score 44; DB 2; Length 534;
Best Local Similarity	88.9%;	Pred. No. 3.2;
Matches	8; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 LQYAFPT 9	
DB	513 LQYRFPYT 521	
RESULT 10		
AD126702		
ID	AD126702 standard; protein; 108 AA.	
XX		
AC	AD126702;	
XX		
DT	15-APR-2004 (first entry)	
DE	Mouse anti Igm antibody HNK-1 kappa light chain protein.	
XX		
XX	Mouse; antibody; Igm; remyelination; neuronal growth; autoantibody;	
KW	demyelination disease; multiple sclerosis; central nervous system; CNS;	
XX	axon; glial cell proliferation;	
KW	Theiler's murine encephalomyelitis virus infection; CNS injury;	
XX	spinal cord injury.	
OS	Mus sp.	
XX		
PN	US2003185827-A1.	
XX		
PD	02-OCT-2003.	

XX 13-NOV-2001; 2001US-00010729.  
PF  
XX 29-APR-1994; 94US-00236520.  
PR 08-AUG-1996; 96US-00692084.  
PR 07-JAN-1997; 97US-0079784.  
PR 28-MAY-1999; 99US-00322862.  
PR 30-MAY-2000; 2000US-00580787.  
PR 05-DEC-2000; 2000US-00730473.  
XX  
PA (MAYO-) MAYO FOUND.  
XX  
PI Rodriguez M, Miller DJ, Pease LR;  
XX  
XX WPI, 2004-119219/12.  
DR N-PSDB; ADI26703.  
XX  
XX New human immunoglobulin M antibody for treating or preventing a  
PT demyelinating disease of the central nervous system in a human or  
PT domestic animal, such as multiple sclerosis.

Example 19, Fig 69, 159pp; English.

XX The invention relates to an antibody (I) produced by injecting an  
CC immunocompetent host with an antibody peptide, and harvesting the  
CC antibody, where the peptide comprises a human anti-IgM antibody fragment  
CC given in the specification, or active fragments. Also included are  
CC stimulating remyelination of central nervous system (CNS) axons in a  
CC mammal (comprising administering a monoclonal antibody, or mixtures,  
CC monomers, active fragments, or recombinant antibodies derived from it,  
CC characterised by their ability to bind structures and cells within the  
CC CNS, including oligodendrocytes), stimulating the proliferation of glial  
CC cells in CNS axons in a mammal (comprising administering a monoclonal  
CC antibody, or mixtures, monomers, active fragments, or recombinant  
CC antibodies derived from it, characterised by their ability to bind  
CC structures and cells within the CNS), treating or preventing a  
CC demyelinating disease of the CNS in a mammal (comprising administering a  
CC monoclonal antibody, or mixtures, monomers, active fragments, or  
CC recombinant antibodies derived from it, characterised by their ability to  
CC bind structures and cells within the CNS, and to stimulate remyelination  
CC of axons of the CNS), stimulating, in vitro, the proliferation of glial  
CC cells from mixed cell culture, stimulating remyelination of CNS axons in  
CC a mammal, a DNA sequence (or degenerate variant of it) which encodes an  
CC antibody/or a peptide analogue, hapten, or active fragment of it, where  
CC the DNA sequence consists of a sequence encoding an anti-IgM antibody), a  
CC probe capable of screening for the antibody, an assay for screening drugs  
CC and other agents for the ability to modulate the production or mimic the  
CC activities of MAB SH1G22, SH1G46, or combinations of them, a  
CC recombinant virus transformed with recombinant antibody nucleic acids or  
CC vector, imaging a portion of the CNS using the antibody and diagnosing or  
CC monitoring demyelination and/or remyelination of the CNS comprising using  
CC CNS image. The antibody is used to stimulate remyelination of CNS axons,  
CC and to stimulate the proliferation of glial cells in CNS axons,  
CC optionally in vitro. The antibody is used to treat or prevent a  
CC demyelinating disease of the CNS in a human or domestic animal, such as  
CC multiple sclerosis, or a disease, other injury or dysfunction of the CNS,  
CC preferably the mammal is a mouse infected with Strain DA of Theiler's  
CC murine encephalomyelitis virus. The antibody is used to treat a spinal  
CC cord injury and used to screen drugs and other agents for the ability to  
CC modulate the production or mimic the activities of the antibody. The  
CC antibody can be used to image a portion of the CNS which can be used to  
CC diagnose or monitor demyelination and/or remyelination of the CNS. The  
CC present sequence is a variable region of a mouse anti-IgM antibody (or  
CC fragment).

XX Sequence 108 AA;

Query Match 87.8%; Score 43; DB 8; Length 108;  
Best Local Similarity 88.9%; Pred. No. 0.93;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYAFPPYT 9  
|||||

Db 89 LOYAFPPYT 97

RESULT 11  
ADE25834  
ID ADE25834 standard; protein; 107 AA.

XX ADE25834;

AC 26-FEB-2004 (first entry)

DE Anti-alpha-v-beta-6 monoclonal Ab light chain variable domain SEQ ID:41.

XX monoclonal antibody; alpha-v-beta-6; latency associated peptide; LAP;  
KW cytotoxic; dermatological; vulnery; hepatotoxic; immunosuppressive;  
KW vaccine; fibrosis; scleroderma; scarring; liver fibrosis;  
XX kidney fibrosis; lung fibrosis; psoriasis; cancer; Alport's syndrome.

OS Synthetic.

XX WO2003100033-A2.

PN 04-DEC-2003.

PD 13-MAR-2003; 2003WO-US008048.

PR 13-MAR-2002; 2002US-0364991P.

PR 13-NOV-2002; 2002US-0426286P.

PA (BIOJ ) BIOGEN INC.

PA (REGC ) UNIV CALIFORNIA.

PI Violette SM, Weinreb PH, Simon KJ, Sheppard D, Leone DR;

XX WPI, 2004-035139/03.

PT New monoclonal antibody that specifically binds to alpha-v-beta-6, and  
PT inhibits the binding of alpha v beta 6 to latency associated peptide  
PT (LAP), useful for treating fibrosis, psoriasis, cancer, or Alport's  
PT syndrome.

XX Claim 27; SEQ ID NO 41; 83pp; English.

XX The present invention describes a monoclonal antibody (I) that  
CC specifically binds to alpha-v-beta-6, and inhibits the binding of alpha-v  
CC -beta-6 to latency associated peptide (LAP) with an IC50 value lower than  
CC that of 10D5. Also described: (1) an anti-alpha-v-beta-6 antibody  
CC comprising heavy chain complementarily determining regions (CDR) 1, 2,  
CC and 3, or a heavy and light chain variable domain sequence; (2) a  
CC monoclonal antibody that specifically binds to alpha-v-beta-6 but does  
CC not inhibit binding of alpha-v-beta-6 to LAP; (3) a composition for  
CC preventing or treating a disease mediated by alpha-v-beta-6 in a mammal  
CC comprising the antibody and a carrier; (4) a method for treating a  
CC subject having or at risk of having a disease mediated by alpha-v-beta-6  
CC by administering to the subject the composition described above, and so  
CC alleviating or postponing the onset of the disease; (5) a method of  
CC detecting alpha-v-beta-6 in a tissue sample by contacting the tissue  
CC sample with the antibody; and (6) a cell hybridoma 6.1A6, 6.3G3, 6.8G6,  
CC 6.2B1, 7.1G10, 7.7G5, or 7.1C7, which respectively comprises American  
CC Type Culture Collection (ATCC) Accession number PTA-3647, PTA-3649, PTA-  
CC 3645, PTA-3646, PTA-3898, PTA-3899, or PTA-3900. (1) has cytosolic,  
CC dermatological, vulnery, hepatotoxic and immunosuppressive activities,  
CC and can be used in vaccines. The antibodies, compositions and methods of  
CC the present invention can be used for preventing or treating a disease  
CC mediated by alpha-v-beta-6, e.g. fibrosis such as scleroderma, scarring,  
CC liver fibrosis, kidney fibrosis or lung fibrosis; psoriasis; cancer,  
CC preferably epithelial cancer, oral, skin, cervical, pharyngeal,  
CC laryngeal, oesophageal, lung, breast, kidney or colorectal cancer; or  
CC Alport's syndrome. The present sequence is used in the exemplification of  
CC the present invention.

XX Sequence 107 AA;

Query Match 83.7%; Score 41; DB 8; Length 107;  
Best Local Similarity 77.8%; Pred. No. 2.3;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQYAFPYT 9  
|||:||||  
DB 89 LQYATPYT 97

RESULT 12  
ADE25833  
ID ADE25833 standard; protein; 107 AA.  
XX ADE25833;  
AC  
DT 26-FEB-2004 (first entry)  
XX  
DE Anti-alpha-v-beta-6 monoclonal Ab light chain variable domain SEQ ID:40.  
XX  
KW monoclonal antibody; alpha-v-beta-6; latency associated peptide; LAP;  
KW cytostatic; dermatological; vulnary; hepatocytic; immunosuppressive;  
KW vaccine; fibrosis; scleroderma; scarring; liver fibrosis;  
KW kidney fibrosis; lung fibrosis; psoriasis; cancer; Alport's syndrome.  
XX  
OS Synthetic.  
XX  
FN WO2003100033-A2.  
XX  
PD 04-DEC-2003.  
XX  
PF 13-MAR-2003; 2003WO-US008048.  
XX  
PR 13-MAR-2002; 2002US-0364991P.  
PR 13-NOV-2002; 2002US-0426286P.  
XX  
PA (BIOJ ) BIOGEN INC.  
PA (RESC ) UNIV CALIFORNIA.  
PI Violante SM, Weinreb PH, Simon KJ, Sheppard D, Leone DR;  
PI, 2004-035139/03.  
DR  
XX MPI, 2004-035139/03.  
XX  
PT New monoclonal antibody that specifically binds to alpha-v-beta-6, and  
PT inhibits the binding of alpha v beta 6 to latency associated peptide  
PT (LAP), useful for treating fibrosis, psoriasis, cancer, or Alport's  
PT syndrome.  
XX  
PS Claim 26; SEQ ID NO 40; 83pp; English.

The present invention describes a monoclonal antibody (1) that specifically binds to alpha-v-beta-6, and inhibits the binding of alpha-v-beta-6 to latency associated peptide (LAP) with an IC50 value lower than that of 10D5. Also described: (1) an anti-alpha-v-beta-6 antibody comprising heavy chain complementarily determining regions (CDR) 1, 2, and 3, or a heavy and light chain variable domain sequence; (2) a monoclonal antibody that specifically binds to alpha-v-beta-6 but does not inhibit binding of alpha-v-beta-6 to LAP; (3) a composition for preventing or treating a disease mediated by alpha-v-beta-6 in a mammal comprising the antibody and a carrier; (4) a method for treating a subject having or at risk of having a disease mediated by alpha-v-beta-6 by administering to the subject the composition described above, and so alleviating or postponing the onset of the disease; (5) a method of detecting alpha-v-beta-6 in a tissue sample by contacting the tissue sample with the antibody; and (6) a cell hybridoma 6.1A8, 6.3G9, 6.8G6, 6.2B1, 7.1G10, 7.7G5, or 7.1CR, which respectively comprises American CC Type Culture Collection (ATCC) Accession number PTA-3647, PTA-3649, PTA-3645, PTA-3646, PTA-3898, PTA-3899, or PTA-3900. (1) has cytostatic, CC dermatological, vulnary, hepatocytic and immunosuppressive activities, CC and can be used in vaccines. The antibodies, compositions and methods of CC the present invention can be used for preventing or treating a disease CC mediated by alpha-v-beta-6, e.g. fibrosis such as scleroderma, scarring, CC liver fibrosis, kidney fibrosis or lung fibrosis; psoriasis; cancer, CC preferably epithelial cancer, oral, skin, cervical, pharyngeal,

CC laryngeal, oesophageal, lung, breast, kidney or colorectal cancer; or  
CC Alport's syndrome. The present sequence is used in the exemplification of  
CC the present invention.  
XX  
SQ Sequence 107 AA;

Query Match 81.6%; Score 40; DB 8; Length 107;  
Best Local Similarity 77.8%; Pred. No. 3.7;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQYAFPYT 9  
|||:||||  
DB 89 LQYATPYT 97

RESULT 13  
AAB60407  
ID AAB60407 standard; peptide; 9 AA.  
XX  
AC AAB60407;  
XX  
DT 24-APR-2001 (first entry)  
XX  
DE ErbB2-reactive VL CDR, SEQ ID NO:12.  
XX  
KW Anti-ErbB2 monoclonal antibody; HER2; humanised; VL;  
KW light chain variable region; cancer; cytostatic; EGFR-expressing cancer;  
KW epidermal growth factor receptor; colon cancer; rectal cancer; tumour;  
KW colorectal cancer; non-small cell lung cancer; metastatic breast cancer;  
KW affinity purification; complementarily determining region; CDR.  
XX  
OS Mus musculus.  
XX  
FN WO200100245-A2.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-US017366.  
XX  
PR 25-JUN-1999; 99US-0141316P.  
XX  
PA (GETH ) GENENTECH INC.  
PI Adams CW, Presta LG, Sliwkowsky M;  
PI, 2001-080862/09.  
DR  
XX MPI, 2001-080862/09.  
XX  
PT Treating cancer in a human, where the cancer expresses epidermal growth  
PT factor receptor (EGFR), comprises administering an antibody which binds  
PT ErbB2.  
XX  
PS Claim 46; Page 66; 89pp; English.

The invention relates to a method for treating cancer in a human patient, wherein the cancer expresses epidermal growth factor receptor (EGFR), comprising administering an antibody which binds ErbB2 (HER2; AAB60408). In particular, the anti-ErbB2 antibody is the murine monoclonal antibody 2C4 (AAB60396, AAB60397) or a humanised version of 2C4 (AAB60398, AAB60399). The invention also encompasses an isolated nucleic acid encoding a humanised ErbB2-binding antibody; vectors and host cells comprising such nucleic acids; the recombinant production of a humanised ErbB2-binding antibody; and an immunocjugate comprising a humanised ErbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies act by antagonising ErbB receptors, and as inhibitors of transforming growth factor alpha (TGF-alpha)-activated mitogen activated protein kinase (MAPK). The method of the invention is used for treating cancer, especially colon cancer, rectal cancer, colorectal cancer, lung cancer, CC (especially non-small cell lung cancer), or breast cancer (especially CC metastatic breast cancer). The antibodies may also have non-therapeutic CC uses e.g., as affinity purification agents. Using an antibody which binds CC to ErbB2 to treat cancer is preferable to the use of EGFR-targeted CC drugs, as EGFR is also highly expressed in other tissues such as the CC liver and skin, where the active drug will also bind, with skin toxicity

CC having been observed for EGFR-targeted drugs. Antibodies which bind  
 CC ErbB2 are anticipated to have a better safety profile than such drugs.  
 CC The present sequence represents a specifically claimed light chain  
 CC variable region (VL) complementarily determining region (CDR) of a  
 CC humanised anti-ErbB2 antibody of the invention  
 CC  
 XX  
 SQ Sequence 9 AA;

Query Match 73.5%; Score 36; DB 4; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIFFPT 9  
 DB 2 QYIYIPYT 9

RESULT 14  
 AAB61592  
 ID AAB61592 standard; peptide; 9 AA.

AC AAB61592;

DT 04-APR-2001 (first entry)

DE Humanised Fab version 574 variable light chain CDR #3.

XX ErbB2; cytosolic; prostate cancer; receptor tyrosine kinase; antibody;  
 XX ErbB receptor; monoclonal antibody 2C4; variable light chain;  
 KW complementarity determining region; CDR.

XX Unidentified.

XX WO200100238-A1.

XX 04-JUN-2001.

XX 23-JUN-2000; 2000WO-US017423.

XX 25-JUN-1999; 99US-0141315P.

XX (GETH ) GENENTECH INC.  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.

XX Agus DB, Scher HI, Sliwkowski MX;

XX WPI; 2001-159131/16.

XX Treating prostate cancer in a human comprises administering an antibody  
 PT which binds ErbB2 and blocks ligand activation of an ErbB receptor.

XX Disclosure; Page 24; 93pp; English.

CC The ErbB family of receptor tyrosine kinases are important mediators of  
 CC cell growth, differentiation and survival. The receptor family includes  
 CC four distinct members including Epidermal Growth Factor Receptor (EGFR or  
 CC ErbB1), HER2 (ErbB2 or p185 neu), HER3 (ErbB3) and Her4 (ErbB4 or tyro2).  
 CC The present invention relates to a method for treating prostate cancer.  
 CC The method comprises administering an antibody which binds ErbB2 and  
 CC blocks ligand activation of an ErbB receptor. Preferably, the antibody  
 CC blocks binding of monoclonal antibody 2C4 to ErbB2 and/or blocks TGF-  
 CC alpha activation of mitogen-activated protein kinase (MAPK). The present  
 CC sequence is a complementarity determining region (CDR) from the variable  
 CC light chain of humanised Fab version 574 antibody  
 CC  
 XX  
 SQ Sequence 9 AA;

Query Match 73.5%; Score 36; DB 4; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIFFPT 9  
 DB 2 QYIYIPYT 9

DB 2 QYIYIPYT 9

RESULT 15  
 AAU76520  
 ID AAU76520 standard; peptide; 9 AA.

AC AAU76520;

DT 05-JUN-2002 (first entry)

DE Anti-Interleukin-12 (IL-12) antibody CDR3 light chain.

XX Human; antibody; anti-interleukin-12; CDR; light chain; circulatory;  
 KW complementarity determining region; neuroprotective; anti-psoriatic;  
 KW immunostimulant; cytosolic; anti-microbial; psoriasis; infection;  
 KW multiple sclerosis; immune disorder; cardiovascular; malignant disease;  
 KW neurological disorder.

XX Homo sapiens.

XX WO200212500-A2.

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US024720.

XX 07-AUG-2000; 2000US-0223358P.

XX 29-SEP-2000; 2000US-0236827P.

XX 01-AUG-2001; 2001US-00920262.

XX (CENZ ) CENTOCOR INC.

XX Giles-Komar J, Knight DM, Perritt D, Scallion B, Shealy D;

XX WPI; 2002-257482/30.

XX New mammalian anti-IL-12 antibodies, useful for diagnosing or treating IL  
 PT -12 related conditions, e.g. psoriasis or multiple sclerosis, as well as  
 PT other for treating immune, infectious, malignant or neurological  
 PT disorders.

XX Claim 41; Page 93; 96pp; English.

CC The invention relates to novel isolated mammalian anti-interleukin-12 (IL  
 CC -12) antibodies. The antibodies comprise at least one complementarity  
 CC determining region (CDR) of a heavy or light chain, a heavy chain or  
 CC light chain variable region, or a heavy chain or light chain constant  
 CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or  
 CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.  
 CC The antibodies are also useful for treating immune, cardiovascular,  
 CC infectious, malignant or neurological disorders or diseases. The present  
 CC sequence represents the amino acid sequence of human anti-interleukin-12  
 CC (IL-12) antibody CDR3 light chain  
 CC  
 XX  
 SQ Sequence 9 AA;

Query Match 73.5%; Score 36; DB 5; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIFFPT 9  
 DB 2 QYIYIPYT 9

Search completed: April 4, 2005, 15:47:18  
 Job time : 18.9712 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 13.2843 Seconds  
(without alignments)  
224.651 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_222\_230  
Perfect score: 49  
Sequence: 1 LQYAFPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues  
Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
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16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	243	9	US-09-887-853-6
2	49	100.0	243	17	US-10-683-547-6
3	49	100.0	267	9	US-09-766-543-10
4	49	100.0	276	9	US-09-766-543-12
5	43	87.8	108	14	US-10-010-729-45
6	39	79.6	217	16	US-10-437-963-119518
7	36	73.5	9	10	US-09-920-262A-6
8	36	73.5	9	14	US-10-268-501-12
9	36	73.5	9	15	US-10-608-626-12
10	36	73.5	9	16	US-10-912-994-6
11	36	73.5	88	16	US-10-437-963-117213
12	36	73.5	107	14	US-10-268-501-1
13	36	73.5	107	14	US-10-268-501-3

14	36	73.5	107	15	US-10-608-626-1	Sequence 1, Appl1
15	36	73.5	107	15	US-10-608-626-3	Sequence 3, Appl1
16	36	73.5	107	15	US-10-600-152-10	Sequence 10, Appl1
17	36	73.5	107	15	US-10-600-152-12	Sequence 12, Appl1
18	36	73.5	107	16	US-10-619-754-1	Sequence 1, Appl1
19	36	73.5	107	16	US-10-619-754-3	Sequence 3, Appl1
20	36	73.5	107	17	US-10-877-532-3	Sequence 3, Appl1
21	36	73.5	108	17	US-09-920-262A-8	Sequence 8, Appl1
22	36	73.5	108	16	US-10-912-994-8	Sequence 8, Appl1
23	36	73.5	109	9	US-09-811-123-4	Sequence 4, Appl1
24	36	73.5	109	9	US-09-811-123-5	Sequence 5, Appl1
25	36	73.5	622	16	US-10-437-963-183264	Sequence 183264,
26	35	71.4	9	9	US-09-861-294-10	Sequence 10, Appl1
27	35	71.4	9	9	US-09-924-099-5	Sequence 5, Appl1
28	35	71.4	9	14	US-10-367-506-10	Sequence 10, Appl1
29	35	71.4	69	14	US-10-106-698-7392	Sequence 7392, Ap
30	35	71.4	94	15	US-10-424-559-270138	Sequence 270138,
31	35	71.4	107	15	US-10-412-703A-12	Sequence 12, Appl1
32	35	71.4	108	9	US-09-924-099-1	Sequence 1, Appl1
33	35	71.4	108	15	US-10-412-703A-6	Sequence 6, Appl1
34	35	71.4	130	8	US-08-779-784-35	Sequence 35, Appl1
35	35	71.4	130	14	US-10-010-729-71	Sequence 71, Appl1
36	35	71.4	145	9	US-09-861-294-2	Sequence 2, Appl1
37	35	71.4	145	14	US-10-367-506-2	Sequence 2, Appl1
38	35	71.4	236	17	US-10-879-994-6	Sequence 6, Appl1
39	35	71.4	237	9	US-09-924-099-9	Sequence 9, Appl1
40	35	71.4	243	9	US-09-924-099-10	Sequence 10, Appl1
41	35	71.4	257	15	US-10-239-656-55	Sequence 55, Appl1
42	35	71.4	257	15	US-10-239-656-67	Sequence 67, Appl1
43	35	71.4	499	15	US-10-239-656-73	Sequence 73, Appl1
44	34	69.4	82	15	US-10-424-559-246038	Sequence 246038,
45	34	69.4	107	15	US-10-389-155-9	Sequence 9, Appl1

## ALIGNMENTS

RESULT 1  
US-09-887-853-6  
Sequence 6, Application US/09887853  
Patent No. US20020168375A1  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
Oppermann, Hermann  
Houston, L. L.  
Ring, David B.  
TITLE OF INVENTION: Biochemical Binding Proteins For Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Testa, Hurwitz & Thibault/Patent Department  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/887,853  
FILING DATE: 21-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/133,804  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:

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;
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 243 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6

Query Match      100.0%; Score 49; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOYALFPYT 9
DB      222 LOYALFPYT 230

RESULT 2
US-10-683-547-6
; Sequence 6, Application US/10683547
; Publication No. US20050058638A1
; GENERAL INFORMATION:
; APPLICANT: Huston, J.
; APPLICANT: Houston, L.L.
; APPLICANT: Ring, D.
; APPLICANT: Oppermann, H.
; TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
; FILE REFERENCE: CIB-P01-130
; CURRENT APPLICATION NUMBER: US/10/683,547
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/09/558,741
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 07/831,967
; PRIOR FILING DATE: 1992-02-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 520C9 sfv
US-10-683-547-6

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Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOYALFPYT 9
DB      222 LOYALFPYT 230

RESULT 3
US-09-766-543-10
; Sequence 10, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwock, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679, 002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
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; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 520C9
; OTHER INFORMATION: humanized single-chain antibody used in the
; OTHER INFORMATION: IL-2-antibody fusions
US-09-766-543-10

Query Match      100.0%; Score 49; DB 9; Length 267;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOYALFPYT 9
DB      241 LOYALFPYT 249

RESULT 4
US-09-766-543-12
; Sequence 12, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwock, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679, 002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: H520C9sfv plus
; OTHER INFORMATION: linker
US-09-766-543-12

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Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOYALFPYT 9
DB      241 LOYALFPYT 249

RESULT 5
US-10-010-729-45
; Sequence 45, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
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; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-45

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Db 89 LOYASFPYT 97

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; Sequence 119518, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 119518
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22728C.1.pep
US-10-437-963-119518

Query Match
Best Local Similarity 79.6%; Score 39; DB 16; Length 217;
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Db 199 YAFPPYT 205

RESULT 7
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; Sequence 6, Application US/09920262A
; Publication No. US20030124123A1
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
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; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-6

Query Match
Best Local Similarity 73.5%; Score 36; DB 10; Length 9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAFPPYT 9
   ||| |||
   ||| |||
Db 2 QYNYFPYT 9

RESULT 8
US-10-268-501-12
; Sequence 12, Application US/10268501
; Publication No. US20030086924A1
; GENERAL INFORMATION:
; APPLICANT: Sliwkowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P1
; CURRENT APPLICATION NUMBER: US/10/268,501
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-268-501-12

Query Match
Best Local Similarity 73.5%; Score 36; DB 14; Length 9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAFPPYT 9
   ||| |||
   ||| |||
Db 2 QYNYFPYT 9

RESULT 9
US-10-608-626-12
; Sequence 12, Application US/10608626
; Publication No. US20040013667A1
; GENERAL INFORMATION:
; APPLICANT: Kelsey, Stephen M.
; APPLICANT: Sliwkowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P2
; CURRENT APPLICATION NUMBER: US/10/608,626
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 10/268,501
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-608-626-12
```

Query Match 73.5%; Score 36; DB 15; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.3e+06;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 OYAIFFYT 9  
Db 2 QYIYIYPT 9

## RESULT 10

US-10-912-994-6  
; Sequence 6, Application US/10912994  
; Publication No. US20050002937A1  
; GENERAL INFORMATION:  
; APPLICANT: Giles-Komar, Jill  
; APPLICANT: Knight, David  
; APPLICANT: Peritt, David  
; APPLICANT: Scallion, Bernie  
; APPLICANT: Shealy, David  
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: CEN0248DIV1  
; CURRENT APPLICATION NUMBER: US/10/912,994  
; CURRENT FILING DATE: 2004-08-06  
; PRIOR APPLICATION NUMBER: US 60/223,358  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 60/236,827  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: US 09/920,262  
; PRIOR FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentln Ver 3.1  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-912-994-6

Query Match 73.5%; Score 36; DB 15; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.3e+06;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 OYAIFFYT 9  
Db 2 QYIYIYPT 9

## RESULT 11

US-10-437-963-137213  
; Sequence 137213, Application US/10437963  
; Publication No. US2004012343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 137213  
; LENGTH: 88  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_38717C.1.pep  
US-10-437-963-137213

Query Match 73.5%; Score 36; DB 16; Length 88;  
Best Local Similarity 85.7%; Pred. No. 28;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VAIFFYT 9  
Db 60 FAIFFYT 66

## RESULT 12

US-10-268-501-1  
; Sequence 1, Application US/10268501  
; Publication No. US20030086924A1  
; GENERAL INFORMATION:  
; APPLICANT: Sliwowski, Mark X.  
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies  
; FILE REFERENCE: P1467R2P1  
; CURRENT APPLICATION NUMBER: US/10/268,501  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 09/602,812  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141,316  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 1  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-10-268-501-1

Query Match 73.5%; Score 36; DB 14; Length 107;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 OYAIFFYT 9  
Db 90 QYIYIYPT 97

## RESULT 13

US-10-268-501-3  
; Sequence 3, Application US/10268501  
; Publication No. US20030086924A1  
; GENERAL INFORMATION:  
; APPLICANT: Sliwowski, Mark X.  
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies  
; FILE REFERENCE: P1467R2P1  
; CURRENT APPLICATION NUMBER: US/10/268,501  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 09/602,812  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141,316  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 3  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized VL sequence  
US-10-268-501-3

Query Match 73.5%; Score 36; DB 14; Length 107;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 OYAIFFYT 9  
Db 90 QYIYIYPT 97

## RESULT 14



US-10-608-626-1  
; Sequence 1, Application US/10608626  
; Publication No. US20040013667A1  
; GENERAL INFORMATION:  
; APPLICANT: Kelsey, Stephen M.  
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies  
; FILE REFERENCE: P1467R2P2  
; CURRENT APPLICATION NUMBER: US/10/608,626  
; CURRENT FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: US 10/268,501  
; PRIOR FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 09/602,812  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141,316  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 1  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-10-608-626-1

Query Match 73.5%; Score 36; DB 15; Length 107;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QYAIFFPT 9  
|||:||||  
Db 90 QYIYFPT 97

RESULT 15  
US-10-608-626-3  
; Sequence 3, Application US/10608626  
; Publication No. US20040013667A1  
; GENERAL INFORMATION:  
; APPLICANT: Kelsey, Stephen M.  
; APPLICANT: Slawkowski, Mark X.  
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies  
; FILE REFERENCE: P1467R2P2  
; CURRENT APPLICATION NUMBER: US/10/608,626  
; CURRENT FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: US 10/268,501  
; PRIOR FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 09/602,812  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141,316  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 3  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanized VL sequence  
US-10-608-626-3

Query Match 73.5%; Score 36; DB 15; Length 107;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QYAIFFPT 9  
|||:||||  
Db 90 QYIYFPT 97

Search completed: April 4, 2005, 16:42:45  
Job time : 13.2843 secs

***This Page Blank (uspio)***

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:32:36 ; Search time 3.2492 Seconds  
(without alignments)  
266.512 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_222\_230  
Perfect score: 49  
Sequence: 1 LQYAFPPYT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	79.6	450	2 F69371	bile acid-inducibl
2	36	73.5	106	2 S20652	Ig kappa chain V r
3	36	73.5	107	2 E64356	conserved hypochet
4	36	73.5	177	2 S62520	hypothetical prote
5	35	71.4	98	2 PH1062	Ig light chain V r
6	35	71.4	101	2 C28840	Ig kappa chain V r
7	35	71.4	101	2 B28840	Ig kappa chain V r
8	35	71.4	106	2 PLO262	Ig kappa chain V r
9	35	71.4	108	1 K1HWE	Ig kappa chain V-I
10	34	69.4	398	2 C71857	probable lipopolys
11	34	69.4	416	2 T50279	hypothetical berin
12	34	69.4	431	2 A64658	LPS biosynthesis p
13	33	67.3	97	2 H84019	hypothetical prote
14	33	67.3	107	2 E83707	hypothetical prote
15	33	67.3	117	2 S42466	Ig kappa chain V r
16	33	67.3	129	2 B23986	Ig kappa chain pre
17	33	67.3	172	2 AB1268	cell-shape determi
18	33	67.3	172	2 AD1630	cell-shape determi
19	33	67.3	242	2 AB3523	taurine transporter
20	33	67.3	642	2 F83718	ABC transporter (A
21	33	67.3	21	2 T28847	hypothetical prote
22	33	67.3	2139	2 S46404	vitellogenin - yel
23	32.5	66.3	723	2 AC1241	polynucleotide pho
24	32.5	66.3	723	2 AG1603	polynucleotide pho
25	32	65.3	106	2 UQ0234	hypothetical 12.5k
26	32	65.3	108	1 K1HUKV	Ig kappa chain V-I
27	32	65.3	112	2 B49060	Ig light chain V r
28	32	65.3	127	2 S52447	Ig kappa chain V r
29	32	65.3	149	2 B69225	hypothetical prote

30	32	65.3	160	2 H86162	hypothetical prote
31	32	65.3	210	2 B81011	glyoxalase II fami
32	32	65.3	218	2 F97021	ABC transporter, p
33	32	65.3	251	2 I40671	flir protein - Cau
34	32	65.3	299	2 G82393	transcription regu
35	32	65.3	331	2 T45089	pyruvate synthase
36	32	65.3	334	2 F75046	pyruvate synthase
37	32	65.3	334	2 F71114	probable ferredoxi
38	32	65.3	371	2 D90192	alcohol dehydrogen
39	32	65.3	401	2 S37815	autochasin A res
40	32	65.3	412	2 T41552	hypothetical prote
41	32	65.3	427	2 F75169	serine hydroxymeth
42	32	65.3	427	2 F71045	probable serine hy
43	32	65.3	458	2 C69406	methylmalonyl-CoA
44	32	65.3	481	2 D75596	UDP-galactose-1-epi
45	32	65.3	508	2 S73859	pyruvate kinase (E

## ALIGNMENTS

### RESULT 1

F69371  
bile acid-inducible operon protein F (baif-2) homolog - Archaeoglobus fulgidus  
C/Species: Archaeoglobus fulgidus  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 03-Jul-2004  
C/Accession: F69371  
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Queckenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirschner, E.F.; Giodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997  
A/Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.A. Smith, H.O.; Woese, C.R.; Venter, J.C.  
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A/Reference number: A69250; MUID:98049343; PMID:9389475  
A/Accession: F69371  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-450 <KLB>  
A/Cross-references: UNIPROT:029288; GB:AE001037; GB:AE000782; NID:G2689360; PIDN:AAB90261

Query Match 79.6% Score 39; DB 2; Length 450;  
Best Local Similarity 85.7% Pred. No. 5.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YAFPPYT 9  
||:||||  
Db 275 YAFPPYT 281

### RESULT 2

S20652  
Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C/Accession: S20652  
R/Losman, M.; Pasy, T.M.; Novick, K.E.; Monestier, M.  
A/Description: Relationships among antinuclear antibodies from autoimmune MRL mice reactj submitted to the EMBL Data Library, February 1992  
A/Reference number: S20639  
A/Accession: S20652  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-106 <LOS>  
A/Cross-references: EMBL:X65008; NID:G52649; PIDN:CAA46141.1; PID:G52650  
C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.5% Score 36; DB 2; Length 106;  
Best Local Similarity 77.8% Pred. No. 5.1;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9  
| | | | |  
Db 89 LOYDDEPYT 97

## RESULT 3

E64356

Conserved hypothetical protein MJ0453 - Methanococcus jannaschii

C/Species: Methanococcus jannaschii

C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2004

C/Accession: E64356

R/Built: C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Bult, C.I.; Overbeek, R.; Kirkness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodek, A.;

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hultsc, M.A.

Science 273, 1058-1073, 1996

A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C

A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A/Reference number: A64300; MUID:96337999; PMID:868087

A/Accession: E64356

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-107 &lt;BUL&gt;

A/Cross-references: UNIPROT:Q57895; GB:U67496; GB:L77117; NID:g2826283; PIDN:AA898442.1;

C/Genetics:

A/Map position: REV405287-404964

C/Superfamily: Uncharacterized conserved protein

Query Match

Best Local Similarity 73.5%; Score 36; DB 2; Length 107;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YALFPYT 9

| | | | |

Db 60 YVIFPYT 66

## RESULT 4

S62520

hypothetical protein SPAC8A4.04c - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe

C/Date: 16-May-1996 #sequence\_revision 13-Mar-1997 #text\_change 31-Jan-2000

C/Accession: T39126; S62520

R/Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, November 1995

A/Reference number: Z21830

A/Accession: T39126

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-177 &lt;LY2&gt;

A/Cross-references: EMBL:Z66569; NID:g1052533; PIDN:CAA91514.1; PID:e207901; PID:g132603

C/Genetics:

A/Gene: SPAC8A4.04c

A/Map position: 1

Query Match

Best Local Similarity 73.5%; Score 36; DB 2; Length 177;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9

| | | | |

Db 163 LOYAVVNYT 171

## RESULT 5

PH1062

Ig light chain V region (clone 202.105) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PH1062

R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B

A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1062  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-98 <TIL>

A/Experimental source: B cell, strain [NZB x NZW]P1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F;16-90/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match

Best Local Similarity 71.4%; Score 35; DB 2; Length 98;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9

| | | | |

Db 89 LOYASSPYT 97

## RESULT 6

C28840

Ig kappa chain V region (HP22) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 21-Jan-2000

C/Accession: C28840; J25114

R/Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.

EMBO J. 4, 3681-3688, 1985

A/Title: The idiotypic network and the internal image: possible regulation of a germ-line

A/Reference number: A91028; MUID:86136012; PMID:3937730

A/Accession: C28840

A/Molecule type: mRNA

A/Residues: 1-101 &lt;OLL&gt;

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;10-84/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match

Best Local Similarity 71.4%; Score 35; DB 2; Length 101;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9

| | | | |

Db 83 LOYASSPYT 91

## RESULT 7

B28840

Ig kappa chain V region (HP27) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 21-Jan-2000

C/Accession: B28840; I25114

R/Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.

EMBO J. 4, 3681-3688, 1985

A/Title: The idiotypic network and the internal image: possible regulation of a germ-line

A/Reference number: A91028; MUID:86136012; PMID:3937730

A/Accession: B28840

A/Molecule type: mRNA

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;10-84/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match

Best Local Similarity 71.4%; Score 35; DB 2; Length 101;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9

| | | | |

Db 83 LOYASSPYT 91

## RESULT 8

PI0262

Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)

C/Species: Mus musculus (house mouse)  
 C/Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
 C/Accession: P10262  
 R/Shlomchik, M.; Masceill, M.; Shan, H.; Radic, M.Z.; Pysereky, D.; Marshak-Rothstein, A.  
 U. Exp. Med. 171, 265-297, 1990  
 A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
 A/Reference number: P10231; MUID:90111618; PMID:2104919  
 A/Accession: P10262  
 A/Molecule type: mRNA  
 A/Residues: 1-106 <SHL>  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 P.1-23/Region: framework 1  
 F.16-90/Domain: immunoglobulin homology <IMM>  
 F.24-34/Region: complementarity-determining 1  
 F.35-49/Region: framework 2  
 F.50-56/Region: complementarity-determining 2  
 F.57-88/Region: framework 3  
 F.89-97/Region: complementarity-determining 3  
 F.98-106/Region: framework 4

Query Match 71.4%; Score 35; DB 2; Length 106;  
 Best Local Similarity 66.7%; Pred. No. 8;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYALFPT 9  
 |||||:  
 Db 89 LOYASFPWT 97

## RESULT 9

KIHWE  
 Ig kappa chain V-I region (WEA) - human

C/Species: Homo sapiens (man)  
 C/Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 09-Jul-2004

C/Accession: A01876

R/Gont, F.; Frangione, B.

Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983

A/Title: Amino acid sequence of the FV region of a human monoclonal IGM (protein WEA) w  
 A/Reference number: A93964; MUID:83237307; PMID:6410398

A/Accession: A01876

A/Molecule type: protein

A/Residues: 1-108 <GON>

A/Cross-references: UNIPROT:P01610  
 C/Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated ga

C/Genetics:

A/Gene: GDB:IGKV1

A/Cross-references: GDB:136264

A/Map position: 2p12-2p12

C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap  
 chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer

F.16-90/Domain: immunoglobulin homology <IMM>  
 F.23-88/Disulfide bonds: #status predicted

Query Match 71.4%; Score 35; DB 1; Length 108;  
 Best Local Similarity 66.7%; Pred. No. 8.2;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYALFPT 9  
 |||||:  
 Db 89 LOYSSFPWT 97

## RESULT 10

C71857  
 Probable lipopolysaccharide biosynthesis protein - Helicobacter pylori (strain J99)

C/Species: Helicobacter pylori  
 A/Variety: strain J99

C/Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
 C/Accession: C71857

R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

; Ives, C.; Gibson, R.; Merberg, D.; Mille, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; 1  
 Nature 397, 176-180, 1999  
 A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho  
 A/Reference number: A71800; MUID:99120557; PMID:9923682  
 A/Accession: C71857  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-398 <ARN>  
 A/Cross-references: UNIPROT:Q9ZXR7; GB:AE001531; GB:AE001439; NID:g4155617; PIDN:AAD0660  
 A/Experimental source: strain J99  
 C/Genetics:  
 A/Gene: jhp1032

Query Match 69.4%; Score 34; DB 2; Length 398;  
 Best Local Similarity 50.0%; Pred. No. 47;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYALFPT 8  
 |||||:  
 Db 212 IEXCVFPY 219

## RESULT 11

T50279

hypothetical serine/threonine repeat protein [imported] - fission yeast (Schizosaccharomy

C/Species: Schizosaccharomyces pombe

C/Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004

C/Accession: T50279

R/Zimmermann, W.; Wambutt, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
 submitted to the EMBL Data Library, January 2000

A/Reference number: Z25053

A/Accession: T50279

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-416 <ZIM>

A/Cross-references: UNIPROT:Q9P329; EMBL:AL137130; PIDN:CAB69629.1; GSPDB:GN00066; SPDB:6

C/Genetics:

A/Gene: SPDB:SPAC977.07C

A/Map position: 1

Query Match 69.4%; Score 34; DB 2; Length 416;  
 Best Local Similarity 55.6%; Pred. No. 49;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYALFPT 9  
 |||||:  
 Db 195 LEYAVYDYT 203

## RESULT 12

A64658  
 LPS biosynthesis protein - Helicobacter pylori (strain 26695)

C/Species: Helicobacter pylori  
 C/Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004

C/Accession: A64658

R/Tomb, J.F.; White, O.; Kurlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;  
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khajak, H.G.; Glodek, A.; McKenney

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.  
 Nature 388, 539-547, 1997

A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.  
 A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A/Reference number: A64520; MUID:97394467; PMID:9252185

A/Accession: A64658

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-431 <TON>

A/Cross-references: UNIPROT:O25733; GB:AE000617; GB:AE000511; NID:g2314256; PIDN:AAD08151

Query Match 69.4%; Score 34; DB 2; Length 431;  
 Best Local Similarity 50.0%; Pred. No. 51;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYAIIPPY 8  
: : : : :  
Db 212 IEYCVFPY 219

## RESULT 13

H84019  
hypothetical protein BH2960 [imported] - Bacillus halodurans (strain C-125)  
C/Species: Bacillus halodurans  
C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C/Accession: H84019  
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A/Reference number: A83650; PMID:20512582; PMID:11058132  
A/Accession: H84019  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-97 <STO>  
A/Cross-references: UNIPROT:Q9K8F3; GB:AP001517; GB:BA000004; NID:G10175500; PIDN:BAB066  
A/Experimental source: strain C-125  
C/Genetics:  
A/Gene: BH2960

Query Match 67.3%; Score 33; DB 2; Length 97;  
Best Local Similarity 75.0%; Pred. No. 18;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYAIIPPY 8  
: : : : :  
Db 37 LEYAIFFAY 44

## RESULT 14

F83707  
hypothetical protein BH0462 [imported] - Bacillus halodurans (strain C-125)  
C/Species: Bacillus halodurans  
C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C/Accession: F83707  
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A/Reference number: A83650; PMID:20512582; PMID:11058132  
A/Accession: F83707  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-107 <STO>  
A/Cross-references: UNIPROT:Q9KFL7; GB:AP001508; GB:BA000004; NID:G10172890; PIDN:BAB041  
A/Experimental source: strain C-125  
C/Genetics:  
A/Gene: BH0462

Query Match 67.3%; Score 33; DB 2; Length 107;  
Best Local Similarity 83.3%; Pred. No. 20;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YAIIPPY 8  
: : : : :  
Db 48 YALFPY 53

## RESULT 15

S42466  
Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C/Accession: S42466  
R/Shiyanov, P.A.; Bespalov, I.A.; Terletskeya, H.N.; Deyev, S.M.  
submitted to the EMBL Data Library, March 1994  
A/Reference number: S42466  
A/Accession: S42466  
A/Status: preliminary  
A/Molecule type: mRNA

A/Residues: 1-117 <SHI>  
A/Cross-references: EMBL:X78108; NID:G460824; PIDN:CAA54998.1; PID:G460825  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/26-100/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 33; DB 2; Length 117;  
Best Local Similarity 62.5%; Pred. No. 22;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIIPPY 9  
: : : : :  
Db 100 QYSSYPY 107

Search completed: April 4, 2005, 15:58:04  
Job time : 5.2492 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 15.2109 Seconds  
(without alignments)  
302.988 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_222\_230  
Perfect score: 49  
Sequence: 1 LOYALFPYT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	83.7	173	2	096YG9 sulfolobus
2	40	81.6	417	2	072ZM4
3	39	79.6	135	2	0654Q7
4	39	79.6	450	2	029288
5	38	77.6	628	2	07RXK3
6	38	77.6	654	2	07S014
7	36	73.5	107	1	Y4S3 METUA
8	36	73.5	274	2	06NCK4
9	36	73.5	276	2	07PEU2
10	36	73.5	300	2	087HF9
11	36	73.5	301	2	06LPM0
12	36	73.5	454	2	098UD2
13	36	73.5	455	1	VEGT_XENTLA
14	36	73.5	455	2	013161
15	36	73.5	455	2	098UD1
16	36	73.5	1366	1	086AM2
17	35	71.4	108	1	KVLR_HUMAN
18	35	71.4	127	2	0925S9
19	35	71.4	173	2	07WTIS
20	35	71.4	233	2	0859G6
21	35	71.4	314	2	07SEL3
22	35	71.4	329	2	061ZJ1
23	35	71.4	347	2	08PR41
24	35	71.4	361	2	086A83
25	35	71.4	442	2	07Q808
26	35	71.4	553	2	024194
27	35	71.4	565	2	09VIC3
28	35	71.4	693	2	095TH0
29	35	71.4	693	2	09VIX4
30	35	71.4	703	2	08SXA1
31	35	71.4	745	2	0747M0

32	35	71.4	879	2	076858	076858 drosophila
33	35	71.4	879	2	09YDC6	09YDC6 drosophila
34	35	71.4	945	2	07R3B3	07R3B3 giardia lam
35	35	71.4	2396	2	07U132	07U132 rhodospirillum
36	34	69.4	325	2	06LQ11	06LQ11 photobacter
37	34	69.4	348	2	06WN37	06WN37 photobacter
38	34	69.4	398	2	09ZKA7	09ZKA7 heliobacter
39	34	69.4	416	2	09P329	09P329 schizosacch
40	34	69.4	425	2	082VZ6	082VZ6 nitrosomon
41	34	69.4	431	2	025733	025733 heliobacte
42	34	69.4	779	2	07S947	07S947 neurospora
43	34	69.4	870	2	081SP3	081SP3 plasmocium
44	33	67.3	79	2	08GR38	08GR38 enterococcu
45	33	67.3	97	2	09K8P3	09K8P3 bacillus ha

## ALIGNMENTS

```
RESULT 1
ID 096YG9 PRELIMINARY; PRT; 173 AA.
AC 096YG9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein ST2202.
GN OrderedlocusNames=ST2202;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_Taxid=11955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / ?
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankal A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kuehida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AF000989; BAB67308.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 173 AA; 19383 MW; 14F1F8AD102BCD CRC64;

Query Match 83.7%; Score 41; DB 2; Length 173;
Best Local Similarity 66.7%; Pred. No. 5.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
Db 120 VRYAVFPYT 128

RESULT 2
ID 072ZM4 PRELIMINARY; PRT; 417 AA.
AC 072ZM4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Vegt.
OS Eleutherodactylus coqui (Puerto Rican coqui).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
OC Telmatobiinae; Eleutherodactylus.
OX NCBI_Taxid=57060;
RN [1]
RP SEQUENCE FROM N.A.
```

```

RA Beckham Y.M., Nath K., Elinson R.P.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY51031; AAP20869.1; -.
DR HSSP; O15119; 1H6F.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53 like DNA_bnd.
DR InterPro; IPR001699; TF_T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS50252; TBOX_3; 1.
SQ SEQUENCE 417 AA; 47815 MW; 23CB46DB5E5E5C09 CRC64;

Query Match
Best Local Similarity 81.6%; Score 39; DB 2; Length 417;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYAFPT 9
Db 408 QYSLFPT 415

RESULT 3
065407 PRELIMINARY; PRT; 135 AA.
AC 065407;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE Hypothetical protein OSUNBA0091G06.4.
GN Name=OSUNBA0091G06.4;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC
clone:OSUNBA0091G06."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF004651; BAD45710.1; -.
KW Hypothetical protein.
SQ SEQUENCE 135 AA; 14500 MW; C2A82C97536D420B CRC64;

Query Match
Best Local Similarity 79.6%; Score 39; DB 2; Length 135;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YAFPT 9
Db 117 YAVFPT 123

RESULT 4
029288 PRELIMINARY; PRT; 450 AA.
AC 029288;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Bile acid-inducible operon protein F (Balf-2).
OS OrderedlocusNames=AF0974;
OC Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.R.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
RA Peterson S.N., Retch C.I., McNeil L.K., Badger J.H., Glodex A.,
RA Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,
RA Ullrich T.R., Cotton M.D., Spriggs T., Artach P., Kaine B.P.,
RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
RA Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
RA Moese C.R., Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
DR EMBL; AE001037; AAB90269.1; -.
DR PIR; F69371; F69371.
DR HSSP; P77407; 1PQY.
DR TIGR; AF0974; -.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR003673; CA1B_BAIF.
DR Pfam; PF02515; COA_transf_3; 1.
KW Complete proteome.
SQ SEQUENCE 450 AA; 51287 MW; 968FC97249CFA8E4 CRC64;

Query Match
Best Local Similarity 79.6%; Score 39; DB 2; Length 450;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YAFPT 9
Db 275 YAVFPT 281

RESULT 5
07RXK3 PRELIMINARY; PRT; 628 AA.
AC 07RXK3;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU03976.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamai M., Kamysseis M., Mauceli E., Bielke C., Rudd S., Frisman D.,
RA Kryzstofova S., Rasmussen C., Metzger R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osman S.A.,
RA Decouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Varden O., Piamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Manthaupt G., Ebbole D.U., Freitag M.,
RA Paulsen I., Sachs W.S., Lander E.S., Nussbaum C., Birren B.;
RT "The genome sequence of the filamentous fungus Neurospora crassa."
RL Nature 0:0-0(2003).
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABX0100743; EAA27327.1; -.
DR HSSP; P22303; 1B41.

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DR GO:0003824; F: catalytic activity; IEA.
DR InterPro; IPR002018; Carbohydraseb.
DR Pfam; PF00135; Coesterase; 1.
DR Hypothetical protein.
SQ SEQUENCE 628 AA; 68076 MW; 0F363A75105971F3 CRC64;

Query Match
Best Local Similarity 77.6%; Score 38; DB 2; Length 628;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYALFPY 8
DB 460 MOYSVFPY 467

RESULT 6
Q7S014 PRELIMINARY; PRT; 654 AA.
AC Q7S014;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU10022.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxId=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR7A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Puccelli S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Erdiczi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Maehurne M.,
RA Seitzmunkoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schlite U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gierre S.,
RA Kamal M., Kamysseila M., Mauceli E., Bielek C., Rudd S., Fishman D.,
RA Kryzocova S., Raamussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Marino G., Catchside D., Li W., Pratt R.J., Osmati S.A.,
RA Desguza C.C., Glas L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Naevig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Frettag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RT Nature 0:0-0(2003).
RL -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX01000496; EAA28821.1; -.
DR HSBP; P22303; 1P8U.
DR GO:0003824; F: catalytic activity; IEA.
DR InterPro; IPR002018; Carbohydraseb.
DR InterPro; IPR003179; Ser_estr.
DR Pfam; PF00135; Coesterase; 1.
DR Hypothetical protein.
SQ SEQUENCE 654 AA; 70515 MW; 99F744A903948390 CRC64;

Query Match
Best Local Similarity 77.6%; Score 38; DB 2; Length 654;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYALFPY 8
DB 466 MOYSVFPY 493

RESULT 7
Y453 METJA STANDARD; PRT; 107 AA.
ID Y453_METJA
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AC Q57895;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical protein MJ0453.
GN OrderedlocusNames=MJ0453;
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxId=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bull C.V., White O., Olsen G.V., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geophagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurec M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Frazer C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073 (1996).

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CC
CC EMBL; U67496; AAB98442.1; -.
DR PIR; E64356; E64356.
DR TIGR; MJ0453; -.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 107 AA; 12603 MW; 4B3723628AEF3F8F CRC64;

Query Match
Best Local Similarity 73.5%; Score 36; DB 1; Length 107;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YALFPYT 9
DB 60 YVIFPYT 66

RESULT 8
Q6NCK4 PRELIMINARY; PRT; 274 AA.
ID Q6NCK4;
AC Q6NCK4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative ATP-binding protein of ABC transporter.
GN OrderedlocusNames=RPA0468;
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiales; Rhodopseudomonas.
OX NCBI_TaxId=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Belletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobet C., Torres y Torres J.L., Perez C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
```

```
CC -1- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
DR EMBL: BX572594; CAE25912.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000515; BPD transp.
DR Pfam: PF00528; BPD transp.1; 1.
DR PROSITE: PS50928; ABC_TML_1.
KW ATP-binding, Complete proteome, Transmembrane, Transport.
SQ SEQUENCE 274 AA; 29247 MW; 1D1088FDD101A759 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 274;
Best Local Similarity 62.5%; Pred. No. 81;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYALFPY 8
DB 102 LEXSLFPY 109

RESULT 9
QY Q7P6U2 PRELIMINARY; PRT; 276 AA.
AC Q7P6U2;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=FN1599;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OC NCBI_TaxID=209882;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49256;
RA Karpstiel V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Watkins T.,
RA Haselkorn R., Overbeek R., Kyriides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABP0100027; EAA24518.1; -.
KW Hypothetical protein.
SQ SEQUENCE 276 AA; 32878 MW; 66E734344433381 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 276;
Best Local Similarity 66.7%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
DB 66 IYLLFPYT 74

RESULT 10
QY Q87HF9 PRELIMINARY; PRT; 300 AA.
AC Q87HF9;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Transcriptional regulator, lysR family.
GN OrderedlocusNames=VPA1006;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
```

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OC Vibrionales; Vibrrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=2508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae."
RL Lancet 361:743-749 (2003).
CC -1- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
DR EMBL: AP005087; BAC62349.1; -.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000847; HTH_LYSR.
DR InterPro: IPR005119; LYSR subet.
DR InterPro: IPR009058; Wing_hlx_DNA_bnd.
DR Pfam: PF00126; HTH_1; 1.
DR Pfam: PF03466; LYSR_substrate; 1.
DR PRINTS: PR00039; HTH_LYSR.
DR PROSITE: PS50931; HTH_LYSR; 1.
KW Complete proteome, DNA-binding, Transcription;
KW Transcription regulation.
SQ SEQUENCE 300 AA; 33894 MW; DDA07EAF2EB68601 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 300;
Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YALFPYT 9
DB 269 YAVFPYT 275

RESULT 11
QY Q6LPN0 PRELIMINARY; PRT; 301 AA.
AC Q6LPN0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical transcriptional regulator, lysR family.
GN Name=VW21654; OrderedlocusNames=PPPR2361;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Viculo N., Lauro F.,
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations."
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR378670; CAG20746.1; -.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000847; HTH_LYSR.
DR InterPro: IPR005119; LYSR subet.
DR InterPro: IPR009058; Wing_hlx_DNA_bnd.
DR Pfam: PF00126; HTH_1; 1.
DR Pfam: PF03466; LYSR_substrate; 1.
DR PROSITE: PS50931; HTH_LYSR; 1.
KW Complete proteome.
SQ SEQUENCE 301 AA; 33862 MW; 3A6D90E214EDA8B0 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 301;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
OY 3 YAIPTPT 9
||:||||
Db 270 YAIPTPT 276

RESULT 12
098UD2 PRELIMINARY; PRT; 454 AA.
AC 098UD2
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Vegt.
GN Name=Vegt;
OS Xenopus borealis (Kenyan clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8354;
RN [1]
RP SEQUENCE FROM N.A.
RA Bubuneko M., Vempati U.D., King M.L.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF180351; AAK00596.1; -.
DR HSP; O15119; IHGF.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53 like DNA_bnd.
DR InterPro; IPR001699; TP_T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS0252; TBOX_3; 1.
SQ SEQUENCE 454 AA; 51855 MW; 4623D860475AD6AC CRC64;

Query Match 73.5%; Score 36; DB 2; Length 454;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 QYAIPTPT 9
||:||||
Db 445 QYSLPPYS 452

RESULT 13
VEGT_XENLA STANDARD; PRT; 455 AA.
ID VEGT_XENLA
AC P87377; P79930; P87386;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE T-box protein VEGT (T-box protein BRAT) (T-box protein antipodean).
GN Name=Vegt; Synonyms=APOD, BRAT;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hord M.E., Thomsen G.H.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RX MEDLINE=97164724; PubMed=9012531;
RA Zhang J., King M.L.;
RT "Xenopus Vegt RNA is localized to the vegetal cortex during oogenesis
and encodes a novel T-box transcription factor involved in mesodermal
```

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RT patterning.";
RL Development 122:4119-4129 (1996).
RN [3]
RP REVISIONS TO 209 AND 396-455.
RN
RA Zhang J., King M.L.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA MEDLINE=97164730; PubMed=9012537;
RA Sternard F., Carnac G., Gurdon J.B.;
RT "The Xenopus T-box gene, Antipodean, encodes a vegetally localised
maternal mRNA and can trigger mesoderm formation.";
RL Development 122:4179-4188 (1996).
CC -1- FUNCTION: Transcription factor involved in mesodermal patterning.
Appears to pattern mesoderm along the dorsoventral and posterior
axis. It activates WNT-8, EOMES and brachyury expression.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Expressed both maternally and zygotically.
Maternally localized to the egg vegetal hemisphere, and in the
developing embryo, in the posterior paraxial mesoderm and ventral
blastopore.
CC -1- DEVELOPMENTAL STAGE: Maternally expressed from early oogenesis.
Zygotic expression occurs from late blastula and reaches maximum
levels during gastrulation (stages 10.5-12). Levels decline at the
time of blastopore closure (stage 13).
CC -1- INDUCTION: By TGF-beta family members.
CC -1- SIMILARITY: Contains 1 T-box domain.
-----
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DR EMBL; U89707; AAB49478.1; -.
DR EMBL; U59483; AAB93301.1; -.
DR EMBL; X99905; CAA68179.1; -.
DR HSP; O15119; IHGF.
DR InterPro; IPR008967; P53 like DNA_bnd.
DR InterPro; IPR001699; TP_T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS0252; TBOX_3; 1.
KW Developmental protein; DNA-binding; Nuclear protein;
Transcription regulation.
FT DNA_BIND 57 230
FT CONFLICT 1 25
FT FT MRNCCRECGLSAGHLEPPASSNCAS -> MHSLP (1in
Ref. 3).
FT SEQUENCE 455 AA; 51795 MW; 9DD12CD704F2AE07 CRC64;

Query Match 73.5%; Score 36; DB 1; Length 455;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 QYAIPTPT 9
||:||||
Db 446 QYSLPPYS 453

RESULT 14
013161 PRELIMINARY; PRT; 455 AA.
ID 013161
AC 013161;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE T-box protein (Xombi protein).
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GN Name=Xombi;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97164713; PubMed=9012520;  
 RA Lusting K.D., Kroll K.L., Sun E.E., Kirschner M.W.;  
 RT "Expression cloning of a Xenopus T-related gene (Xombi) involved in  
 RL mesodermal patterning and blastopore lip formation.";  
 Dev. Biol. 122:4001-4012 (1996).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Oocytes;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.P., Hsieh F.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.D., Abramson R.D., Mallari S.J.,  
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Myers R.M., Butterfield J.S.,  
 RA Krzywinski M.I., Skalska U., Smalius D.E., Schmech A., Schein J.E.,  
 RA Jones S.J., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Oocytes;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.,  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT Initiative.";  
 Dev. Dyn. 225:384-391 (2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Oocytes;  
 RA Klein S., Strausberg R.,  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; S83518; AAB50917.1; -.  
 DR EMBL; BC070708; AAF070708.1; -.  
 DR HSSP; O15119; 1H6F.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR008967; P53\_like\_DNA\_bnd.  
 DR InterPro; IPR001699; TF\_T-box.  
 DR Pfam; PF00907; T-box; 1.  
 DR PRINTS; PR00937; TBOX.  
 DR SMART; SM00425; TBOX; 1.  
 DR PROSITE; PS01283; TBOX\_1; 1.  
 DR PROSITE; PS01264; TBOX\_2; 1.  
 DR PROSITE; PS50252; TBOX\_3; 1.  
 SQ SEQUENCE 455 AA; 51963 MW; 2B9C8FBCCD7B37D CRC64;

DB 446 QYSLFPYS 453

RESULT 15  
 ID 098UD1 PRELIMINARY; PRT; 455 AA.  
 AC 098UD1;  
 DT 01-UN-2001 (TREMBLrel. 17, Created)  
 DT 01-UN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE VegT.  
 GN Name=VegT;  
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8364;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bubnerko M., Vempati U.D., King M.L.;  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF180352; AAK00597.1; -.  
 DR HSSP; O15119; 1H6F.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR008967; P53\_like\_DNA\_bnd.  
 DR InterPro; IPR001699; TF\_T-box.  
 DR Pfam; PF00907; T-box; 1.  
 DR PRINTS; PR00937; TBOX.  
 DR SMART; SM00425; TBOX; 1.  
 DR PROSITE; PS01283; TBOX\_1; 1.  
 DR PROSITE; PS01264; TBOX\_2; 1.  
 DR PROSITE; PS50252; TBOX\_3; 1.  
 SQ SEQUENCE 455 AA; 51890 MW; 0D2502AF91CBA2B0 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 455;  
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYALPPT 9  
 DB 446 QYSLFPYS 453

Search completed: April 4, 2005, 15:56:19  
 Job time : 20.2109 secs

QY 2 QYALPPT 9  
 ||::|||:

Query Match 73.5%; Score 36; DB 2; Length 455;  
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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## OM protein - protein search, using sw model

Run on: April 4, 2005, 15:19:49 ; Search time 9.98403 seconds  
(without alignments)  
193.690 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_31\_35  
Perfect score: 30  
Sequence: 1 NYGMN 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq.16dec04:\*  
1: geneeqp1980a:\*  
2: geneeqp1990a:\*  
3: geneeqp2000a:\*  
4: geneeqp2001a:\*  
5: geneeqp2002a:\*  
6: geneeqp2003a:\*  
7: geneeqp2003ba:\*  
8: geneeqp2004a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	5	2	AAR85496
2	30	100.0	5	2	AAW24504
3	30	100.0	5	3	AAV32223
4	30	100.0	5	3	AAU80973
5	30	100.0	5	7	ABR61517
6	30	100.0	5	8	ADG34365
7	30	100.0	5	8	ADL23057
8	30	100.0	5	8	ADL23057
9	30	100.0	5	8	ADL23057
10	30	100.0	5	8	ADL23057
11	30	100.0	5	8	ADL23057
12	30	100.0	5	8	ADL23057
13	30	100.0	5	8	ADL23057
14	30	100.0	5	8	ADL23057
15	30	100.0	5	8	ADL23057
16	30	100.0	5	8	ADL23057
17	30	100.0	5	8	ADL23057
18	30	100.0	5	8	ADL23057
19	30	100.0	5	8	ADL23057
20	30	100.0	5	8	ADL23057
21	30	100.0	5	8	ADL23057
22	30	100.0	5	8	ADL23057
23	30	100.0	5	8	ADL23057
24	30	100.0	5	8	ADL23057
25	30	100.0	5	8	ADL23057

## ALIGNMENTS

26	30	100.0	92	2	AAW24529	AAW24529	Anti-Fact
27	30	100.0	92	2	AAU80997	AAU80997	Human ant
28	30	100.0	112	2	AAW24521	AAW24521	Anti-Fact
29	30	100.0	112	5	AAU80980	AAU80980	Human ant
30	30	100.0	115	3	AAV90823	AAV90823	520C9 hyb
31	30	100.0	115	4	AAW84740	AAW84740	Variable
32	30	100.0	116	4	AAW84739	AAW84739	Variable
33	30	100.0	116	5	AAE27830	AAE27830	Mouse KS
34	30	100.0	116	5	AAE27839	AAE27839	Mouse KS
35	30	100.0	116	5	AAE27837	AAE27837	Mouse KS
36	30	100.0	116	5	AAE27825	AAE27825	Mouse KS
37	30	100.0	116	5	AAE27826	AAE27826	Mouse KS
38	30	100.0	116	5	AAE27828	AAE27828	Mouse KS
39	30	100.0	116	5	AAE27832	AAE27832	Mouse KS
40	30	100.0	116	5	AAE27834	AAE27834	Mouse KS
41	30	100.0	116	5	ADG67541	ADG67541	KS antibo
42	30	100.0	116	5	ADG67537	ADG67537	KS antibo
43	30	100.0	116	5	ADG67543	ADG67543	KS antibo
44	30	100.0	116	5	ADG67531	ADG67531	KS antibo
45	30	100.0	116	5	ADG67533	ADG67533	KS antibo

RESULT 1  
AAR85496  
ID AAR85496 standard; peptide; 5 AA.  
XX  
AC AAR85496;  
XX  
DT 16-MAR-1996 (first entry)  
XX  
DE SCFV(FRP)5 CDR1H.  
XX  
KW Single chain antibody; scFv; antibody engineering; antitumour;  
KW tumour antigen binding; cytotoxic T-lymphocyte; cell targeting;  
KW monoclonal antibody; erB-2; cancer; adoptive immunotherapy;  
KW complementarity determining region; CDR.  
XX  
OS Synthetic.  
XX  
PN WO9530014-A1.  
XX  
PD 09-NOV-1995.  
XX  
PF 20-APR-1995; 95WO-EP001494.  
XX  
PR 02-MAY-1994; 94EP-00810244.  
XX  
PA (CIBA ) CIBA GEIGY AG.  
XX  
PI Groner B, Moritz D;  
XX WPI, 1995-393085/50.  
XX  
PT New bifunctional proteins for use in killing tumour cells - contg. a  
PT tumour antigen binding domain, a hinge region and a zeta chain derived  
PT from a T-cell antigen receptor.  
XX  
PS Disclosure; Page 6; 46pp; English.  
XX  
CC Complementarity determining regions (CDRs) CDR1H, CDR2H and CDR3H  
CC (AAR85496-98) and CDR1L, CDR2L and CDR3L (AAR85502-04) are components of  
CC the heavy chain variable region and light chain variable region,  
CC respectively, of single chain antibody scFv(FRP)5 (AAR85494). The CDRs  
CC are derived from mouse monoclonal antibody FRP5 (EGACC 90112115). The  
CC scFv is specific for the extracellular domain of erB-2, and is used as  
CC the tumour antigen binding domain of a bifunctional protein that is  
CC expressed in cytotoxic T-lymphocytes (CTLs), allowing adoptive  
CC immunotherapy of cancer  
XX  
SQ Sequence 5 AA:

Query Match 100.0%; Score 30; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
 |||||  
 Db 1 NYGMN 5

RESULT 2  
 AAM24504  
 ID AAM24504 standard; peptide; 5 AA.  
 XX  
 AC AAM24504;  
 XX  
 DT 26-DEC-1997 (first entry)  
 XX  
 DE Mouse anti-human Factor IX antibody BC2 heavy chain CDR1.

XX Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;  
 KM humanised antibody; antibody engineering; heavy chain; CDR;  
 KM complementarity determining region; myocardial infarction; angina;  
 KM atrial fibrillation; stroke; kidney damage; pulmonary embolism;  
 KM deep vein thrombosis; coronary angioplasty; pulmonary embolism;  
 KM disseminated intravascular coagulation; artificial organ; sepsis; shunt;  
 KM prostheses.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO9726010-A1.  
 XX  
 PD 24-JUL-1997.  
 XX  
 PF 17-JAN-1997; 97WO-US000759.  
 XX  
 PR 17-JAN-1996; 96US-0010108P.  
 PR 24-OCT-1996; 96US-0029119P.  
 XX  
 PI (SMIRK) SMITHKLINE BEECHAM CORP.  
 XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
 PA Blackburn MN, Church WR, Feuerstein GZ, Gross MS, Nichols AJ;  
 PI Padlan EA, Patel AH, Sylvester DR;  
 DR WPI; 1997-385117/35.  
 XX  
 PT Inhibiting thrombosis with self-limiting antibody to coagulation factor -  
 PT avoids uncontrolled bleeding by providing only partial inhibition.  
 XX  
 PS Claim 21; Page 65; 150pp; English.

XX This peptide comprises complementarity determining region 1 (CDR1) of the  
 CC heavy chain variable region (VH) of mouse anti-human Factor IX monoclonal  
 CC antibody BC2 (see also AAM24519). Claimed humanised antibodies (see  
 CC AAM24510-18) contain CDRs (see AAM24504-09) of BC2 VH and VL inserted  
 CC into framework regions of selected human antibody sequences. They have  
 CC self-limiting neutralising activity, and are useful as anticoagulant  
 CC agents in treatment of thrombosis associated with myocardial infarct,  
 CC unstable angina, atrial fibrillation, stroke, renal damage, pulmonary  
 CC embolism, deep vein thrombosis, percutaneous transluminal coronary  
 CC angioplasty, disseminated intravascular coagulation, sepsis, or  
 CC artificial organs, shunts or prostheses (claimed). Also claimed are  
 CC chimeric antibodies, as well as Fab and Fab'2 fragments. The claimed  
 CC antibodies do not cause uncontrolled bleeding (contrast heparin and  
 CC warfarin) since they provide only partial inhibition of coagulation  
 CC  
 XX

Sequence 5 AA:

Query Match 100.0%; Score 30; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
 |||||  
 Db 1 NYGMN 5

RESULT 3  
 AAY32223  
 ID AAY32223 standard; peptide; 5 AA.  
 XX  
 AC AAY32223;  
 XX  
 DT 15-FEB-2000 (first entry)  
 XX  
 DE G-CSF agonist antibody mAb163-93 heavy chain variable region CDR1.

XX Granulocyte colony stimulating factor receptor; G-CSF; mouse;  
 KM monoclonal antibody; agonist; screening; neutropenia; therapy;  
 KM complementarity determining region; CDR; mAb163-93.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO9955735-A1.  
 XX  
 PD 04-NOV-1999.  
 XX  
 PF 30-APR-1999; 99WO-US009466.  
 XX  
 PR 30-APR-1998; 98US-0083575P.  
 XX  
 PA (TANO-) TANOX INC.  
 XX  
 PI Ni B, Sun BNC, Sun CRF;  
 XX  
 DR WPI; 2000-052805/04.  
 XX  
 PT Treatment of neutropenia by stimulating proliferation of neutrophilic  
 PT cell lineage progenitors.  
 XX  
 PS Claim 13; Page 30; 64pp; English.

XX The present sequence represents complementarity determining region 1  
 CC (CDR1) of the heavy chain variable region of murine monoclonal antibody  
 CC mAb163-93. This antibody is an example of an agonist molecule that  
 CC specifically binds to or interacts with human granulocyte colony  
 CC stimulating factor (G-CSF) receptor to stimulate cell proliferation and  
 CC differentiation, especially by dimerising with the receptor or activating  
 CC phosphorylation of kinases associated with the receptor. Agonist  
 CC antibodies can be used to stimulate proliferation of G-CSF-dependent  
 CC cells, e.g. to differentiate leading to a repopulation of neutrophilic  
 CC granulocyte lineage cells, especially to treat neutropenia (claimed).  
 CC They can also be used to detect human G-CSF receptor immunologically  
 CC  
 XX

Sequence 5 AA:

Query Match 100.0%; Score 30; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
 |||||  
 Db 1 NYGMN 5

RESULT 4  
 AAU80973  
 ID AAU80973 standard; peptide; 5 AA.  
 XX  
 AC AAU80973;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Murine BC2 heavy chain variable region CDR1.

XX

KW Human; mouse; BC2; animal post-thromboembolic induced ischaemia;  
KW thrombolytic agent; anti-factor IX antibody; plasminogen activator;  
KW thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic;  
KW vasotropic; cardiac; anti-respiratory syncytial virus;  
KW heavy chain variable region; light chain variable region.  
OS Mus sp.  
XX WO200187339-A1.  
PN 22-NOV-2001.  
XX 05-OCT-2000; 2000WO-US027438.  
PF 15-MAY-2000; 2000US-00571434.  
PR (SMIK ) SMITHKLINE BEECHAM CORP.  
XX Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR;  
PI WPI; 2002-082944/11.  
XX Treating post-thromboembolic induced ischemia in an animal by  
PT administering anti-factor IX antibody in combination with a plasminogen  
PT activator.  
XX Example 5; Page 95; 163pp; English.  
PS The invention relates to a method for treating an animal post-  
CC thromboembolic induced ischemia or reducing a required dose of a  
CC thrombolytic agent in treatment of an animal post-thromboembolic induced  
CC ischaemia, comprising administering an anti-factor IX antibody or its  
CC fragment, optionally in combination with a plasminogen activator or  
CC thrombolytic agent. The method is useful for treating post-thromboembolic  
CC -induced ischaemia, for preventing thromboembolic stroke in an animal,  
CC and for reducing a required dose of a thrombolytic agent. Sequences  
CC AAU80972-AAU81004 represent antibodies and vector polypeptides used in  
CC the method of the invention  
XX Sequence 5 AA;  
SQ  
Query Match 100.0%; Score 30; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
DB 1 NYGMN 5  
RESULT 5  
ABR61517  
ID ABR61517 standard; peptide; 5 AA.  
XX ABR61517;  
AC ABR61517;  
XX 15-JAN-2004 (first entry)  
DT 15-JAN-2004 (first entry)  
XX Humanised RS7 antibody heavy chain variable region CDR1 fragment.  
DE Humanised RS7 antibody heavy chain variable region CDR1 fragment.  
XX EGP-1; glycoprotein; cytosolic; antigen binding protein; cancer;  
KW RS7 antibody; complementarily determining region; CDR.  
XX Homo sapiens.  
OS WO2003074566-A2.  
XX 12-SEP-2003.  
PD 03-MAR-2003; 2003WO-GB000885.  
PF 01-MAR-2002; 2002US-0360229P.  
PR 01-MAR-2002; 2002US-0360229P.  
XX

PA (IMMU-) IMMUNOMEDICS INC.  
PA (MCCA/) MCCALL J D.  
XX Govindan S, Qu Z, Hansen HJ, Goldenberg DM;  
PI WPI; 2003-767380/72.  
XX Monovalent and multivalent humanized RS7 antigen binding proteins useful  
PT in the diagnosis and therapy of cancer.  
PT Claim 6; Page 65; 97pp; English.  
PS The invention relates to an antibody (Ab) or fragment that binds to an  
CC EGP-1 glycoprotein. The methods are useful for delivering a diagnostic or  
CC therapeutic composition, diagnosing or treating cancer, treating a  
CC malignancy, and treating a cancer cell. A therapeutic conjugate or  
CC diagnostic conjugate comprising EGP-1 Mab, a fragment of an antibody  
CC fusion protein or fragment is used for the diagnosis or treatment of a  
CC malignancy when bound to at least one therapeutic agent. The diagnostic/  
CC therapeutic agent or a combination of both comprising at least one Ab are  
CC used for targeting an EGP-1 target antigen on a cell. The cancers are  
CC lung, ovarian, prostate, colon, stomach, bladder and breast cancer. Naked  
CC anti-EGP-1 Mab or fragment is used for the treatment of cancer. The  
CC invention provides multivalent, monospecific binding proteins that are  
CC useful in a direct targeting system and for production of multivalent,  
CC multispecific binding proteins that are useful in an affinity enhancement  
CC system. The present sequence represents a humanised anti-EGP-1 antibody  
CC heavy chain variable region CDR1 fragment  
XX Sequence 5 AA;  
SQ  
Query Match 100.0%; Score 30; DB 7; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
DB 1 NYGMN 5  
RESULT 6  
ADG34365  
ID ADG34365 standard; peptide; 5 AA.  
XX ADG34365;  
AC ADG34365;  
XX 26-FEB-2004 (first entry)  
DT 26-FEB-2004 (first entry)  
XX Humanised mouse BAT-1 antibody-derived HC variable region seqID9.  
DE Humanised mouse BAT-1 antibody-derived HC variable region seqID9.  
XX humanised monoclonal antibody; complementarily determining region; CDR;  
KW murine monoclonal antibody BAT-1; mBAT-1; framework region; PR;  
KW acceptor human immunoglobulin; anti-cumour; immunogenic; cytostatic;  
KW anti-HIV; immunotherapy; cancer; HIV infection; autoimmune disorder;  
KW immune deficiency; mouse; murine; heavy chain variable region.  
XX Mus sp.  
OS WO2003099196-A2.  
XX 04-DEC-2003.  
PD 22-MAY-2003; 2003WO-IL000425.  
PF 23-MAY-2002; 2002IL-00149820.  
PR (CURE-) CURE TECH LTD.  
XX (MORR-) MOR RES APPL LTD.  
PA Hardy B, Jones ST, Klapper L;  
PI WPI; 2004-035027/03.  
DR WPI; 2004-035027/03.  
XX

PT New humanized monoclonal antibody having a complementarity determining  
PT region of murine monoclonal antibody B2T-1 and a framework region from  
PT an acceptor human immunoglobulin, useful for treating cancer or early  
PT stages of HIV.  
XX  
PS Claim 4; SEQ ID NO 12; 145bp; English.  
XX  
CC This invention relates to a novel humanised monoclonal antibody having at  
CC least one complementarity determining region (CDR) of murine monoclonal  
CC antibody B2T-1 (MB2T-1) and a framework region (FR) derived from an  
CC acceptor human immunoglobulin. The humanised antibody retains the anti-  
CC tumour activity of MB2T-1 monoclonal antibody and is less immunogenic in  
CC a human subject than the murine antibody. The invention may be useful in  
CC the development of compounds with a cytostatic or anti-HIV activity. The  
CC human monoclonal antibodies are useful in immunotherapy, particularly for  
CC treating cancer. The antibodies are also useful for treating early stages  
CC of HIV infection or in patients whose blood count shows a decrease in  
CC autoimmune disorders, or in some cases of genetic or acquired immune  
CC deficiencies.  
XX  
SQ Sequence 5 AA;  
XX  
Query Match 100.0%; Score 30; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
OY 1 NYGMN 5  
Db 1 NYGMN 5  
XX  
RESULT 7  
ADL23057  
ID ADL23057 standard; peptide; 5 AA.  
XX  
AC ADL23057;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Myelin associated glycoprotein MAG binding antibody heavy chain CDR H1.  
XX  
XX antibody; MAG; myelin associated glycoprotein; heavy chain; CDR; stroke;  
XX neurodegenerative disorder; gene therapy; vaccine.  
XX  
OS Unidentified.  
XX  
PN WO2004014953-A2.  
XX  
PD 19-FEB-2004.  
XX  
PF 05-AUG-2003; 2003WO-BP008749.  
XX  
PR 06-AUG-2002; 2002GB-00018229.  
XX  
PR 06-AUG-2002; 2002GB-00018230.  
XX  
PR 06-AUG-2002; 2002GB-00018232.  
XX  
PR 06-AUG-2002; 2002GB-00018234.  
XX  
PA (GLAXO ) GLAXO GROUP LTD.  
XX  
PI Ellis JH, Gernaschewski V;  
XX  
DR WPI; 2004-180641/17.  
XX  
DR N-PSDB; ADL23034.  
XX  
XX New altered antibody that binds to and neutralizes myelin associated  
XX glycoprotein (MAG), useful for preparing a composition for treating or  
XX preventing stroke or other neurodegenerative disorders e.g., Alzheimer's  
XX disease.  
XX  
XX Claim 1; Page 53; 67pp; English.  
XX  
XX The present invention relates to a new altered antibody or its functional  
XX fragment, which binds to and neutralizes myelin associated glycoprotein

CC (MAG) and comprises a light chain variable domain (VL) comprising  
CC complementary determining region light 1 (CDRL1), CDRL2 or CDRL3 and/or a  
CC heavy chain variable domain (VH) comprising CDRL1, CDRL2 or CDRL3. The  
CC antibody is useful for preparing a composition for treating or preventing  
CC stroke or other neurodegenerative disorders in a human, e.g., traumatic  
CC brain injury, Alzheimer's disease, dementias, peripheral neuropathy,  
CC Parkinson's disease, Huntington's disease and multiple sclerosis. The  
CC present sequence is the anti-MAG antibody heavy chain CDR H1 of the  
CC invention.  
XX  
SQ Sequence 5 AA;  
XX  
Query Match 100.0%; Score 30; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
OY 1 NYGMN 5  
Db 1 NYGMN 5  
XX  
RESULT 8  
ADS87336  
ID ADS87336 standard; peptide; 5 AA.  
XX  
AC ADS87336;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Humanised antibody MN3 heavy chain variable region CDRL1.  
XX  
XX  
XX cyostatic; vasotropic; antimicrobial; antiinflammatory; antipyretic;  
XX antiatherosclerotic; cardiac; monoclonal antibody; NCA90; NCA95;  
XX chimeric antibody; humanized antibody; inflammation; appendicitis;  
XX inflammatory bowel disease; pelvic inflammatory disease; fever;  
XX cystic fibrosis; granulocyte related disorder; atherosclerosis;  
XX infarction; cancer; ischemic lesion; complementarity determining region.  
XX  
OS Homo sapiens.  
OS Mus sp.  
OS Chimeric.  
XX  
PN WO2004029093-A2.  
XX  
PD 08-APR-2004.  
XX  
PF 30-SEP-2003; 2003WO-GB004229.  
XX  
PR 30-SEP-2002; 2002US-0414341P.  
XX  
PR (IMMU-) IMMUNOMEDICS INC.  
XX  
PA (MCCA/) MCCALL J D.  
XX  
PI Goldenberg DM, Hansen H, Leung S;  
XX  
DR WPI; 2004-329873/30.  
XX  
XX Monoclonal anti-granulocyte antibody that binds NCA90 and NCA95 antigens,  
XX useful for treating malignancy, inflammation, atherosclerosis,  
XX infarction, or other granulocyte related disorders.  
XX  
XX Claim 4; Page 105; 134pp; English.  
XX  
XX The invention relates to a monoclonal antibody (Mab) (I) or its fragment  
XX that binds NCA90 or NCA95, where when the Mab or its fragment binds NCA90  
XX the Mab or its fragment is chimeric, partially humanized or fully  
XX humanized and where when the Mab or its fragment binds NCA95 the Mab or  
XX its fragment is either fully humanized or chimeric, partially humanized  
XX or fully humanized BW 250/183. (II) is useful for treating, detecting or  
XX imaging sites of inflammation resulting from appendicitis, inflammatory  
XX bowel disease, pelvic inflammatory disease, fever and cystic fibrosis and  
XX treating granulocyte related disorders, atherosclerosis and infarction.  
XX  
XX (I) is useful for detecting or treating cancer or ischemic lesion. This



CC sequence corresponds to the complementarity determining region 1 (CDR1)  
XX of the heavy chain of the antibody of the invention.

8Q Sequence 5 AA;

Query Match 100.0%; Score 30; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
| | | | |  
DB 1 NYGMN 5

RESULT 9  
ADS88789

ID ADS88789 standard; peptide; 5 AA.

AC ADS88789;

DT 16-DEC-2004 (first entry)

DE Heavy chain CDR H1 of an anti-MAG antibody.

XX oligodendrocyte; stroke; neurological disease;  
XX myelin-associated glycoprotein; MAG; anti-MAG antibody;  
XX Alzheimer's disease; multiple sclerosis;  
XX chain complementarity determining region; CDR.

OS Unidentified.

PN WO2004083363-A2.

PD 30-SEP-2004.

PF 02-FEB-2004; 2004WO-EP001016.

PR 19-MAR-2003; 2003GB-00006309.

PA (GLAX ) GLAXO GROUP LTD.

PI Vinson M, Irving EA;

DR WPI; 2004-691029/67.

XX Promoting oligodendrocyte survival in humans with neurological diseases,  
PT such as Alzheimer's disease, multiple sclerosis and/or stroke, using an  
PT anti-myelin-associated glycoprotein (MAG) antibody.

PS Claim 6; SEQ ID NO 4; 45bp; English.

XX The specification describes a method for promoting oligodendrocyte  
CC survival in a human suffering or at risk of developing stroke or another  
CC neurological disease. The method comprises administering to the human an  
CC anti-myelin-associated glycoprotein (MAG) antibody or its functional  
CC fragment. The anti-MAG antibody or its functional fragment is useful in  
CC the manufacture of a medicament for the promotion of oligodendrocyte  
CC survival in a human suffering from or at risk of developing stroke or  
CC another neurological disease. They can also be used in treating  
CC neurological diseases, such as Alzheimer's disease, multiple sclerosis  
CC and/or stroke, by promoting oligodendrocyte survival. ADS88789-ADS88791  
CC represent the heavy chain complementarity determining regions (CDRs) of  
CC an anti-MAG antibody which can be used in the method of the invention.

XX Sequence 5 AA;

Query Match 100.0%; Score 30; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
| | | | |  
DB 1 NYGMN 5

RESULT 10  
AAB99237

ID AAB99237 standard; peptide; 6 AA.

AC AAB99237;

DT 10-SEP-2001 (first entry)

DE Mouse clone 13 CDR1 peptide.

XX Cytostatic; immunostimulation; antibody; H11; tumour; cancer; murine;  
XX antigen-binding fragment; stress protein-peptide complex; SPCC; CDR;  
XX complementarity determining region.

OS Mus sp.

PN WO200140292-A1.

PD 07-JUN-2001.

PF 29-NOV-1999; 99WO-CA001141.

PR 29-NOV-1999; 99WO-CA001141.

PA (NOVO-) NOVOPHARM BIOTECH INC.

PI Dan M, Entwistle J, Fast D, Kaplan H, Lewis K, Macdonald G;  
PI Maltz P;

DR WPI; 2001-356155/37.

XX Antigen-binding fragments specific for stress protein-peptide complexes  
PT (SPCCs) associated with tumors and cancer associated SPCCs, useful for  
PT treating a range of cancers.

PS Example 23; Page 133; 176pp; English.

XX The present invention relates to antigen-binding fragments, which are  
CC specific for stress protein-peptide complexes (SPCCs) associated with  
CC tumours and cancer associated SPCCs. The cancer-specific SPCC complexes  
CC are useful for initiating cancer-specific immunogenic responses against a  
CC variety of cancers: astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
CC oligodendroglioma, ependymoma, medulloblastoma, primitive neural  
CC ectodermal tumour (PNET), chondrosarcoma, osteogenic sarcoma, pancreatic  
CC ductal adenocarcinoma, small and large cell lung adenocarcinomas,  
CC choriona, angiosarcoma, endotheliosarcoma, squamous cell carcinoma,  
CC bronchoalveolarcarcinoma, epithelial adenocarcinoma, and liver metastases  
CC thereof, lymphangiosarcoma, lymphangioidendotheliosarcoma, hepatoma,  
CC cholangiocarcinoma, synovialoma, mesothelioma, Ewing's tumour,  
CC rhabdomyosarcoma, colon carcinoma, basal cell carcinoma, sweat gland  
CC carcinoma, papillary carcinoma, sebaceous gland carcinoma, papillary  
CC adenocarcinoma, cystadenocarcinoma, medullary carcinoma, bronchogenic  
CC carcinoma, renal cell carcinoma, bileduct carcinoma, choriocarcinoma,  
CC seminoma, embryonal carcinoma, Wilms' tumour, testicular tumour,  
CC craniopharyngioma, pinealoma, hemangioblastoma, acoustic neuroma, kidney  
CC adenocarcinoma, meningioma, neuroblastoma, retinoblastoma, leukaemia,  
CC multiple myeloma, Waldenstrom's macroglobulinaemia, and heavy chain  
CC disease, breast tumours such as ductal and lobular adenocarcinoma,  
CC squamous and adenocarcinomas of the uterine cervix, uterine and ovarian  
CC epithelial carcinomas, prostatic adenocarcinomas, transitional squamous  
CC cell carcinoma of the bladder, B and T cell lymphomas (nodular and  
CC diffuse) plasmacytoma, acute and chronic leukaemias, malignant melanoma,  
CC glioblastoma, colon adenocarcinoma, small cell lung carcinoma, soft  
CC tissue sarcomas, ovarian adenocarcinoma, ovarian adenocarcinoma, bladder  
CC cell carcinoma, prostate adenocarcinoma, larynx carcinoma and  
CC leiomyosarcomas. The present sequence is a complementarity determining  
CC region (CDR) peptide from mouse clone 13, which was used in an example  
CC from the present invention. Mouse clone 13 was derived via mouse scfv  
CC library panning against SPCC H11, for the isolation of binders to the  
CC antigen. Mouse clone 13 was found to show specific binding to SPCC

SQ Sequence 6 AA;  
Query Match 100.0%; Score 30; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
Db 2 NYGMN 6  
RESULT 11  
ID AAY17489 standard; peptide; 7 AA.  
AC AAY17489;  
DT 03-AUG-1999 (first entry)  
DE Mab 31.1 CDR sequence derived peptide COL11 H1.  
XX Heavy chain variable region; 2CAVHCOL1; light chain variable region;  
XX light chain consensus region; heavy chain consensus region; antibody;  
XX anti-idiotypic response; modified immunoglobulin; infectious disease;  
XX cancer; vaccine.  
XX Synthetic.  
XX WO9925379-A1.  
XX 27-MAY-1999.  
XX 13-NOV-1998; 98WO-US024303.  
XX 14-NOV-1997; 97US-0065716P.  
XX 10-APR-1998; 98US-0081403P.  
XX (EURO-) EUROCELLTICQUE SA.  
XX Burch RM;  
XX WPI; 1999-337877/28.  
XX Vaccines for generating an anti-idiotypic response to an antigen.  
XX Example; Page 55; 107pp; English.  
XX The present invention describes vaccines for generating an anti-idiotypic  
XX response to an antigen. Vaccine (A), comprises, apart from a carrier, a  
XX first immunoglobulin (I), comprising a variable region (V), or its  
XX fragment that includes V, which is identical to a second immunoglobulin  
XX (II), or its corresponding fragment, which can bind specifically to an  
XX antigen (Ag), except for one or more amino acid (aa) substitutions in V.  
XX These substitutions involve replacement of Cys residues involved in  
XX disulfide bridge formation by residues that do not contain a thiol group.  
XX (A) are used to raise an anti-idiotypic response (preferably both cellular  
XX and humoral), particularly for treating a wide range of tumours (or  
XX precancerous conditions) and infectious diseases (viral, bacterial,  
XX fungal, parasitic), specifically syphilis, gonorrhea, acquired immune  
XX deficiency syndrome, malaria, Shigella, Salmonella, hepatitis A or C,  
XX Lyme disease, encephalitis, herpes, Gram-positive or -negative bacterial  
XX infections, or pneumococcal infections. Antibodies raised against the  
XX vaccine may be recovered and administered to a second subject. (I) may  
XX also be used for treating autoimmune diseases and allergy. Modifying (II)  
XX so that it can no longer form intrachain disulfide bridges reduces  
XX conformational constraints and results in significantly better anti-  
XX idiotypic responses. The present sequence represents a Mab 31.1 CDR  
XX sequence derived peptide from an example from the present invention  
XX Sequence 7 AA;  
Query Match 100.0%; Score 30; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
Db 3 NYGMN 7  
RESULT 12  
ID AAY08698 standard; protein; 7 AA.  
AC AAY08698;  
DT 10-AUG-1999 (first entry)  
DE Human colon carcinoma-associated protein antigen binding fragment 4.  
XX Immunoglobulin; immunospecific; variable domain; CDR; cancer antigen;  
XX complementarity determining region; infectious disease agent antigen;  
XX cellular receptor; infectious agent; chemotherapeutic agent; vaccine;  
XX cancer; infectious disease; autoimmune disease; rheumatoid arthritis;  
XX ulcerative colitis; psoriasis; allergy; immunoassay reagent; diagnosis;  
XX veterinary medicine; antibody; immunisation; antibody; immune tolerance;  
XX human colon cancer-associated protein antigen; cryptic expression;  
XX anti-idiotypic immune response.  
XX Homo sapiens.  
XX WO9925378-A1.  
XX 27-MAY-1999.  
XX 13-NOV-1998; 98WO-US024302.  
XX 14-NOV-1997; 97US-0065716P.  
XX 10-APR-1998; 98US-0081403P.  
XX (EURO-) EUROCELLTICQUE SA.  
XX Burch RM;  
XX WPI; 1999-357555/30.  
XX Modified immunoglobulins including engineered binding site.  
XX Claim 6; Page 75; 123pp; English.  
XX This invention describes a novel modified immunoglobulin (mig), or its  
XX fragment, that binds immunospecifically to one member (M1) of a binding  
XX pair comprises a variable domain (V) having at least one CDR  
XX (complementarity determining region) that contains a portion of the  
XX second member (M2) of the pair. This portion is not present in the  
XX natural CDR and M1 is a cancer antigen, infectious disease agent antigen,  
XX a cellular receptor for an infectious agent (provided the binding site is  
XX not NAMP or NUDP) or a member of a receptor-ligand pair. mig (also  
XX related molecules containing the same V region), optionally coupled to a  
XX chemotherapeutic agent, are used in therapeutic and/or prophylactic  
XX compositions, or vaccines, against cancer, infectious or autoimmune  
XX diseases (rheumatoid arthritis, ulcerative colitis or psoriasis) or  
XX allergies. They can also be used as immunoassay reagents for diagnosing  
XX these conditions. mig can be used in human or veterinary medicine. mig  
XX have higher affinity or specificity than native antibodies. Manipulation  
XX of CDR ensures binding specificity and avoids the unpredictable  
XX immunisation and screening procedures currently used. It is now possible  
XX to generate antibodies against antigens that are inaccessible, by virtue  
XX of immune tolerance or cryptic expression. mig neutralize antigens  
XX directly or they induce an anti-idiotypic immune response. This sequence  
XX represents a fragment of modified immunoglobulin that immunospecifically  
XX binds to a binding pair in which the first member is the human colon  
XX carcinoma-associated protein antigen  
XX Sequence 7 AA;



```

XX
AC AAG80311;
XX
DT 18-FEB-2002 (first entry)
XX
DE Anti-human TNF-alpha CDR-H1 peptide.
XX
KW TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KW heavy chain; light chain; complementarity determining region; vasotropic;
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KW rheumatoid arthritis; malaria; multiple sclerosis.
XX
OS Homo sapiens.
XX
PN WO200179298-A1.
XX
PD 25-OCT-2001.
XX
PF 18-APR-2001; 2001WO-JP003308.
XX
PR 19-APR-2000; 2000JP-00117394.
XX
PA (SUNR ) SUNTORX LTD.
XX
PI Fukuda Y, Nagahira K, Nakanishi T;
XX
DR WPI; 2002-066345/09.
XX
PT Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.
XX
PS Claim 1a; Page 25; 36pp; Japanese.
XX
CC This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarily determining region (CDR) sequences. The products
CC of the invention have vasotropic, antiarthritic, neuroprotective and
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in
CC vivo. The antibodies are used for producing chimeric and humanised
CC antibodies that may be used for the treatment and prevention of TNF-alpha
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC humans. This sequence represents the anti-human tumour necrosis factor-
CC alpha (TNF-alpha) heavy chain CDR1 designated CDR-H1
XX
SQ Sequence 10 AA;

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Query Match 100.0%; Score 30; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.1;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 NYGMN 5
   |||||
Db 6 NYGMN 10

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Search completed: April 4, 2005, 15:47:07  
 Job time : 11.984 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 7.38019 Seconds  
(without alignments)  
224.651 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_31\_35  
Perfect score: 30  
Sequence: 1 NYGMN 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	5	9	US-09-965-099-8
2	30	100.0	5	10	US-09-791-551-74
3	30	100.0	5	13	US-10-051-852-8
4	30	100.0	5	14	US-10-071-962-15
5	30	100.0	5	15	US-10-430-176-8
6	30	100.0	5	15	US-10-377-121-26
7	30	100.0	10	9	US-09-056-1608-1
8	30	100.0	10	14	US-10-234-671-1
9	30	100.0	10	16	US-10-018-245A-1
10	30	100.0	10	16	US-10-723-434-111
11	30	100.0	10	16	US-10-723-434-112
12	30	100.0	10	16	US-10-723-434-116
13	30	100.0	10	16	US-10-723-434-122

14	30	100.0	10	17	US-10-687-035-60	Sequence 60, Appl
15	30	100.0	12	10	US-09-954-385-147	Sequence 147, App
16	30	100.0	12	17	US-10-912-512-147	Sequence 147, App
17	30	100.0	12	17	US-10-235-043-147	Sequence 147, App
18	30	100.0	67	14	US-10-243-130-19	Sequence 19, Appl
19	30	100.0	70	14	US-10-243-130-17	Sequence 17, Appl
20	30	100.0	70	14	US-10-243-130-18	Sequence 18, Appl
21	30	100.0	70	17	US-10-901-650-17	Sequence 17, Appl
22	30	100.0	70	17	US-10-901-650-18	Sequence 18, Appl
23	30	100.0	70	17	US-10-901-650-19	Sequence 19, Appl
24	30	100.0	76	15	US-10-424-559-268610	Sequence 268610,
25	30	100.0	92	13	US-09-965-099-84	Sequence 84, Appl
26	30	100.0	92	13	US-10-051-852-84	Sequence 84, Appl
27	30	100.0	92	15	US-10-430-176-84	Sequence 84, Appl
28	30	100.0	112	9	US-09-965-099-20	Sequence 20, Appl
29	30	100.0	112	13	US-10-051-852-20	Sequence 20, Appl
30	30	100.0	112	15	US-10-430-176-20	Sequence 20, Appl
31	30	100.0	116	9	US-09-971-543-8	Sequence 9, Appl
32	30	100.0	116	9	US-09-971-543-9	Sequence 9, Appl
33	30	100.0	116	9	US-09-971-543-10	Sequence 10, Appl
34	30	100.0	116	14	US-10-138-727A-2	Sequence 2, Appl
35	30	100.0	116	14	US-10-138-727A-4	Sequence 4, Appl
36	30	100.0	116	14	US-10-138-727A-6	Sequence 6, Appl
37	30	100.0	116	14	US-10-138-727A-17	Sequence 17, Appl
38	30	100.0	116	14	US-10-138-727A-18	Sequence 18, Appl
39	30	100.0	116	14	US-10-138-727A-19	Sequence 19, Appl
40	30	100.0	116	14	US-10-138-727A-20	Sequence 20, Appl
41	30	100.0	116	14	US-10-138-727A-21	Sequence 21, Appl
42	30	100.0	116	14	US-10-138-727A-22	Sequence 22, Appl
43	30	100.0	116	14	US-10-138-727A-23	Sequence 23, Appl
44	30	100.0	116	14	US-10-138-727A-24	Sequence 24, Appl
45	30	100.0	116	14	US-10-138-727A-25	Sequence 25, Appl

#### ALIGNMENTS

RESULT 1  
US-09-965-099-8  
; Sequence 8, Application US/09965099  
; Patent No. US20020136725A1  
; GENERAL INFORMATION:  
; APPLICANT: Blackburn, Michael  
; Feuerstein, Girola  
; Patel, Arunbhai  
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN  
; TREATMENT OF THROMBOSIS  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/965, 099  
; FILING DATE: 26-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/346,487  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baumeister, Kirk  
; REGISTRATION NUMBER: 33,833  
; REFERENCE/DOCKET NUMBER: P50438-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5096

TELEFAX: <Unknown>  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-965-099-8

Query Match 100.0%; Score 30; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 1 NYGMN 5

RESULT 2  
US-09-791-551-74  
Sequence 74, Application US/09791551  
Publication No. US20030235584A1  
GENERAL INFORMATION:  
APPLICANT: KLOETZER, WILLIAM S.  
APPLICANT: HANNA, NABIL  
TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES  
FILE REFERENCE: 037003/0277869  
CURRENT APPLICATION NUMBER: US/09/791,551  
CURRENT FILING DATE: 2001-02-26  
PRIOR APPLICATION NUMBER: 60/185,390  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: 60/233,625  
PRIOR FILING DATE: 2000-09-18  
NUMBER OF SEQ ID NOS: 119  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 74  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Mus sp.  
US-09-791-551-74

Query Match 100.0%; Score 30; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 1 NYGMN 5

RESULT 3  
US-10-051-852-8  
Sequence 8, Application US/10051852  
Publication No. US20020146411A1  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
Church, William  
Gross, Mitchell  
Feuerstein, Giora  
Nichols, Andrew  
Padlan, Eduardo  
Patel, Arunbhai  
Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/051,852  
FILING DATE: 17-Jan-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/344,050  
FILING DATE: 25-JUN-1999  
APPLICATION NUMBER: 08/783,853  
FILING DATE: 16-JAN-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX: <Unknown>

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-10-051-852-8

Query Match 100.0%; Score 30; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 1 NYGMN 5

RESULT 4  
US-10-071-962-15  
Sequence 15, Application US/10071962  
Publication No. US20030170237A1  
GENERAL INFORMATION:  
APPLICANT: Bault N.  
APPLICANT: Bault N.C. Sun  
APPLICANT: Cedilly R.Y. Sun  
TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and  
TITLE OF INVENTION: Screening Method Therefor  
FILE REFERENCE: 98-3  
CURRENT APPLICATION NUMBER: US/10/071,962  
CURRENT FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US/09/303,155A  
PRIOR FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: 60/083,575  
PRIOR FILING DATE: 1998-04-30  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 5

TYPE: PRT  
ORGANISM: mouse  
US-10-071-962-15.

Query Match 100.0%; Score 30; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
DB 1 NYGMN 5

RESULT 5  
US-10-430-176-8  
Sequence 8, Application US/10430176  
Publication No. US20030235587A1  
GENERAL INFORMATION:

APPLICANT: Feuerstein, Gloria Z.  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
FILE REFERENCE: P50816-1  
CURRENT APPLICATION NUMBER: US/10/430,176  
CURRENT FILING DATE: 2003-05-05  
PRIOR APPLICATION NUMBER: 09/817,960  
PRIOR FILING DATE: 2001-03-27  
PRIOR APPLICATION NUMBER: 09/359,202  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 60/095,714  
PRIOR FILING DATE: 1998-08-07  
PRIOR APPLICATION NUMBER: 10/051,852  
PRIOR FILING DATE: 2002-01-17  
PRIOR APPLICATION NUMBER: 09/344,050  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: 08/783,853  
PRIOR FILING DATE: 1997-01-06  
PRIOR APPLICATION NUMBER: 60/010,018  
PRIOR FILING DATE: 199-01-17  
PRIOR APPLICATION NUMBER: 60/029,119  
PRIOR FILING DATE: 1996-10-24  
NUMBER OF SEQ ID NOS: 111  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Home sapiens  
US-10-430-176-8

Query Match 100.0%; Score 30; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
DB 1 NYGMN 5

RESULT 6  
US-10-377-121-26  
Sequence 26, Application US/10377121  
Publication No. US20040001825A1  
GENERAL INFORMATION:  
APPLICANT: GOVINDAM, SERENGULAM  
APPLICANT: GU, ZHENGXING  
APPLICANT: HANSEN, HANS  
APPLICANT: GOLDENBERG, DAVID  
TITLE OF INVENTION: RS7 ANTIBODIES  
FILE REFERENCE: 018733/1163  
CURRENT APPLICATION NUMBER: US/10/377,121  
CURRENT FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: 60/360,299  
PRIOR FILING DATE: 2002-03-01  
NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 26  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Mus sp.  
US-10-377-121-26

Query Match 100.0%; Score 30; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
DB 1 NYGMN 5

RESULT 7  
US-09-056-160B-1  
Sequence 1, Application US/09056160B  
Patent No. US20020032315A1  
GENERAL INFORMATION:

APPLICANT: Baca, Manuel  
APPLICANT: Wells, James A.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Lowman, Henry B.  
APPLICANT: Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,160B  
FILING DATE: 06-Apr-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/054,856  
FILING DATE: 06-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1093R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-056-160B-1

Query Match 100.0%; Score 30; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
DB 6 NYGMN 10

RESULT 8  
US-10-234-671-1  
Sequence 1, Application US/10234671

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/ Publication No. US20030190317A1
/ GENERAL INFORMATION:
/ APPLICANT: Baca, Manuel
/               Wells, James A.
/               Presta, Leonard G.
/               Lowman, Henry B.
/               Chen, Yvonne M.
/ TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
/ NUMBER OF SEQUENCES: 131
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSER: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/234,671
/ FILING DATE: 03-Sep-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/056160
/ FILING DATE: 06-APR-1998
/ APPLICATION NUMBER: 60/126446
/ FILING DATE: 07-APR-1997
/ APPLICATION NUMBER: 60/054856
/ FILING DATE: 06-AUG-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cui, Steven X.
/ REGISTRATION NUMBER: 44,637
/ REFERENCE/DOCKET NUMBER: P1093R2C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-8674
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
/ US-10-234-671-1

Query Match      100.0%; Score 30; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYGMN 5
        |||||
Db      6 NYGMN 10

RESULT 9
US-10-018-245A-1
/ Sequence 1, Application US/10018245A
/ Publication No. US20040115196A1
/ GENERAL INFORMATION:
/ APPLICANT: FUKUDA, Yoshiaki
/ APPLICANT: NAKAHARA, Kazuhiko
/ APPLICANT: NAKANISHI, Toshihiro
/ TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement
/ TITLE OF INVENTION: determining regions and genes encoding the same
/ FILE REFERENCE: 46224
/ CURRENT APPLICATION NUMBER: US/10/018,245A
/ CURRENT FILING DATE: 2002-07-12
/ PRIOR APPLICATION NUMBER: JP 117394/2000
/ PRIOR FILING DATE: 2000-04-19
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatencIn Ver. 2.1
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```
/ SEQ ID NO: 1
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: mouse
/ FEATURE:
/ OTHER INFORMATION: CDR-H1 of anti-human TNF-alpha antibody
/ US-10-018-245A-1

Query Match      100.0%; Score 30; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYGMN 5
        |||||
Db      6 NYGMN 10

RESULT 10
US-10-723-434-111
/ Sequence 111, Application US/10723434
/ Publication No. US2004013357A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhong, Pingyu
/ APPLICANT: Luo, Peizhi
/ APPLICANT: Wang, Kevin C.
/ APPLICANT: Hsieh, Mark
/ APPLICANT: Li, Yan
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
/ FILE REFERENCE: 26050-709,501
/ CURRENT APPLICATION NUMBER: US/10/723,434
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: US 60/284,407
/ PRIOR FILING DATE: 2001-04-17
/ PRIOR APPLICATION NUMBER: US 10/125,687
/ PRIOR FILING DATE: 2002-04-17
/ PRIOR APPLICATION NUMBER: US 10/153,176
/ PRIOR FILING DATE: 2002-05-20
/ PRIOR APPLICATION NUMBER: US 10/443,134
/ PRIOR FILING DATE: 2003-05-20
/ NUMBER OF SEQ ID NOS: 156
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 111
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VH/CDR1
/ US-10-723-434-111

Query Match      100.0%; Score 30; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYGMN 5
        |||||
Db      6 NYGMN 10

RESULT 11
US-10-723-434-112
/ Sequence 112, Application US/10723434
/ Publication No. US2004013357A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhong, Pingyu
/ APPLICANT: Luo, Peizhi
/ APPLICANT: Wang, Kevin C.
/ APPLICANT: Hsieh, Mark
/ APPLICANT: Li, Yan
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
/ FILE REFERENCE: 26050-709,501
/ CURRENT APPLICATION NUMBER: US/10/723,434
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: US 60/284,407
```



PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: US 10/125,687  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: US 10/153,176  
PRIOR FILING DATE: 2002-05-20  
PRIOR APPLICATION NUMBER: US 10/443,134  
PRIOR FILING DATE: 2003-05-20  
NUMBER OF SEQ ID NOS: 156  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 112  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VH/CDRI  
US-10-723-434-112

Query Match 100.0%; Score 30; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 6 NYGMN 10

RESULT 12  
US-10-723-434-116  
Sequence 116, Application US/10723434  
Publication No. US2004013357A1  
GENERAL INFORMATION:  
APPLICANT: Zhong, Pingyu  
APPLICANT: Luo, Peizhi  
APPLICANT: Wang, Kevin C.  
APPLICANT: Hsieh, Mark  
APPLICANT: Li, Yan  
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR  
FILE REFERENCE: 26050-709, 501  
CURRENT APPLICATION NUMBER: US/10/723,434  
CURRENT FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: US 60/284,407  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: US 10/125,687  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: US 10/153,176  
PRIOR FILING DATE: 2002-05-20  
PRIOR APPLICATION NUMBER: US 10/443,134  
NUMBER OF SEQ ID NOS: 156  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 116  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VH/CDRI  
US-10-723-434-116

Query Match 100.0%; Score 30; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 6 NYGMN 10

RESULT 13  
US-10-723-434-122  
Sequence 122, Application US/10723434  
Publication No. US2004013357A1  
GENERAL INFORMATION:  
APPLICANT: Zhong, Pingyu

APPLICANT: Luo, Peizhi  
APPLICANT: Wang, Kevin C.  
APPLICANT: Hsieh, Mark  
APPLICANT: Li, Yan  
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR  
FILE REFERENCE: 26050-709, 501  
CURRENT APPLICATION NUMBER: US/10/723,434  
CURRENT FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: US 60/284,407  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: US 10/125,687  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: US 10/153,176  
PRIOR FILING DATE: 2002-05-20  
PRIOR APPLICATION NUMBER: US 10/443,134  
NUMBER OF SEQ ID NOS: 156  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 122  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VH/CDRI  
US-10-723-434-122

Query Match 100.0%; Score 30; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 6 NYGMN 10

RESULT 14  
US-10-687-035-60  
Sequence 60, Application US/10687035  
Publication No. US20050064518A1  
GENERAL INFORMATION:  
APPLICANT: Albane, Earl F.  
APPLICANT: Solcic, Daniel A.  
TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED  
FILE REFERENCE: 6750-214-999  
CURRENT APPLICATION NUMBER: US/10/687,035  
CURRENT FILING DATE: 2003-10-15  
PRIOR APPLICATION NUMBER: 60/485,986  
PRIOR FILING DATE: 2003-07-10  
PRIOR APPLICATION NUMBER: 60/418,828  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 60  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 725.1 VH1 CDR  
US-10-687-035-60

Query Match 100.0%; Score 30; DB 17; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 6 NYGMN 10

RESULT 15  
US-09-954-385-147  
Sequence 147, Application US/09954385

/ Publication No. US20030100467A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Aehle, Wolfgang  
/ APPLICANT: Baldwin, Toby L.  
/ APPLICANT: Van Gastel, Franciscus J.C.  
/ APPLICANT: Janssen, Giselie G. J.  
/ APPLICANT: Murray, Christopher J.  
/ APPLICANT: Wang, Huaming  
/ APPLICANT: Winetzk, Deborah S.  
/ TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
/ TITLE OF INVENTION: Complexes  
/ FILE REFERENCE: GC690  
/ CURRENT APPLICATION NUMBER: US/09/954,385  
/ CURRENT FILING DATE: 2001-09-12  
/ NUMBER OF SEQ ID NOS: 433  
/ SOFTWARE: FastSeq For Windows Version 4.0  
/ SEQ ID NO 147  
/ LENGTH: 12  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: binding peptide  
US-09-954-385-147

Query Match 100.0%; Score 30; DB 10; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||  
Db 6 NYGMN 10

Search completed: April 4, 2005, 16:42:43  
Job time : 8.38019 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: April 4, 2005, 15:32:36 ; Search time 1.80511 seconds

(without alignments)  
266.512 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_31\_35

Perfect score: 30

Sequence: 1 NYGMN 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR79: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	93	2 C24672	Ig heavy chain V r
2	30	100.0	99	2 S26326	Ig heavy chain V r
3	30	100.0	101	2 D24672	Ig heavy chain V r
4	30	100.0	105	2 S24764	Ig heavy chain V r
5	30	100.0	105	2 S24765	Ig heavy chain V r
6	30	100.0	109	2 S26325	Ig heavy chain V r
7	30	100.0	115	2 S19968	Ig heavy chain V r
8	30	100.0	115	2 S19965	Ig heavy chain V r
9	30	100.0	116	2 S63305	Ig heavy chain V r
10	30	100.0	118	2 S19967	Ig heavy chain V r
11	30	100.0	119	2 A53285	Ig heavy chain V a
12	30	100.0	120	2 B42848	Ig mb heavy chain
13	30	100.0	120	2 S12953	Ig heavy chain V r
14	30	100.0	124	2 PH1404	Ig heavy chain V r
15	30	100.0	146	4 S33905	Ig heavy chain pre
16	30	100.0	398	2 B90406	geranylgeranyl hyd
17	30	100.0	725	2 S01042	aerobactin recepto
18	30	100.0	726	2 AB0122	probable ferric si
19	30	100.0	732	2 T44483	receptor-like prot
20	27	90.0	96	2 B90793	hypothetical prote
21	27	90.0	96	2 G85653	hypothetical prote
22	27	90.0	151	2 E70615	hypothetical prote
23	27	90.0	153	2 G75616	hypothetical prote
24	27	90.0	174	2 P85028	modulation protein
25	27	90.0	191	2 A97074	hypothetical prote
26	27	90.0	212	2 D84442	probable glutathio
27	27	90.0	281	2 S34496	hypothetical prote
28	27	90.0	321	2 D97836	tetraacyldisacchar
29	27	90.0	326	1 VGXR37	glycoprotein VP7 p

30	27	90.0	326	1 VGXR7H	glycoprotein VP7 p
31	27	90.0	326	1 VGXRMD	glycoprotein VP7 p
32	27	90.0	326	1 VGXRWA	glycoprotein VP7 p
33	27	90.0	329	2 T13016	hypothetical prote
34	27	90.0	338	2 T28779	hypothetical prote
35	27	90.0	340	2 T28080	hypothetical prote
36	27	90.0	344	2 H45252	ply constant regi
37	27	90.0	373	2 A69143	galactosyl-transfe
38	27	90.0	381	2 T40341	hypothetical prote
39	27	90.0	388	2 A82903	conserved hypotet
40	27	90.0	391	2 E83840	hypothetical prote
41	27	90.0	406	2 JCA600	isocitrate dehydro
42	27	90.0	454	2 A97147	siderophore/Surfac
43	27	90.0	470	1 S14628	phosphogluconate d
44	27	90.0	560	2 S09995	nuclear factor I-B
45	27	90.0	561	2 A31256	transcription fact

## ALIGNMENTS

## RESULT 1

C24672 Ig heavy chain V region (VMU-1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 23-Jul-1999

C/Accession: C24672

R/Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A/Reference number: A91022; MUID:86055722; PMID:2998759

A/Accession: C24672

A/Molecule type: DNA

A/Residues: 1-93 &lt;MIN&gt;

A/Cross-references: GB:X03300; NID:952375; PIDN:CAA27039.1; PID:g773221

A/Note: this sequence was determined from the differentiated gene

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 30; DB 2; Length 93;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 12 NYGMN 16

## RESULT 2

S26326 Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1998 #sequence\_revision 19-Mar-1998 #text\_change 17-Apr-1998

C/Accession: S26326

R/Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A/Title: Antibodies that are specific for a single amino acid interchange in a protein ei

A/Reference number: S26309; MUID:91341421; PMID:1908510

A/Accession: S26326

A/Molecule type: mRNA

A/Residues: 1-99 &lt;STA&gt;

A/Cross-references: EMBL:X59174

A/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 30; DB 2; Length 99;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 11 NYGMN 15

## RESULT 3

D24672

Ig heavy chain V region (VGM3-8) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 23-Jul-1999

C/Accession: D24672

R/Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A/Reference number: A91022; MUID:86055722; PMID:2998759

A/Accession: D24672

A/Molecule type: DNA

A/Residues: 1-101 &lt;MIN&gt;

A/Cross-references: GB:X03301; NID:G51757; PIDN:CAA27040.1; PID:G773215

A/Note: this sequence was determined from the differentiated gene

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 30; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 12 NYGMN 16

## RESULT 4

S24764

Ig heavy chain V region (subgroup XI) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999

C/Accession: S24764; S24772; S24777

R/Klages, S.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24763

A/Accession: S24764

A/Molecule type: DNA

A/Residues: 1-105 &lt;KLA&gt;

A/Cross-references: EMBL:Z14999

A/Accession: S24772

A/Molecule type: DNA

A/Residues: 1-105 &lt;KLM&gt;

A/Cross-references: EMBL:Z15011

R/Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24776

A/Accession: S24777

A/Molecule type: DNA

A/Residues: 1-105 &lt;THO&gt;

A/Cross-references: EMBL:Z15020; NID:G52616; PIDN:CAA78739.1; PID:G52617

C/Genetics: 9/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 30; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 43 NYGMN 47

## RESULT 5

S24765

Ig heavy chain V region (subgroup XI) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999

C/Accession: S24765; S24773; S24778

R/Klages, S.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24763

A/Accession: S24765

A/Molecule type: DNA

A/Residues: 1-105 &lt;KLA&gt;

A/Cross-references: EMBL:Z15001

A/Accession: S24773

A/Molecule type: DNA

A/Residues: 1-105 &lt;KLM&gt;

A/Cross-references: EMBL:Z15013

R/Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24776

A/Accession: S24778

A/Molecule type: DNA

A/Residues: 1-105 &lt;THO&gt;

A/Cross-references: EMBL:Z15022; NID:G52619; PIDN:CAA78741.1; PID:G52620

C/Genetics: 9/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 30; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 43 NYGMN 47

## RESULT 6

S26325

Ig heavy chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C/Accession: S26325

R/Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A/Title: Antibodies that are specific for a single amino acid interchange in a protein ef

A/Reference number: S26309; MUID:91341421; PMID:1908510

A/Accession: S26325

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-109 &lt;STA&gt;

A/Cross-references: UNIPROT:Q921A6; EMBL:X59210; NID:G52080; PID:G1334043

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/5-88/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 100.0%; Score 30; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 21 NYGMN 25

## RESULT 7

S19968

Ig heavy chain V region (M-T408) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004

C/Accession: S19968

R/Weissenborn, W.; Riettmüller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A/Description: Structural characterization of CD4 mAb.

A/Reference number: S19963

A/Accession: S19968

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-115 &lt;WEI&gt;

A/Cross-references: UNIPROT:Q921A6; EMBL:X65089

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin  
P:10-93/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
DB 26 NYGMN 30

RESULT 8  
S19965

Ig heavy chain V region (M-T321) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S19965

R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mAb.

A:Reference number: S19963

A:Accession: S19965

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-115 <WEI>

A:Cross-references: UNIPROT:Q921A6; EMBL:X65088

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

P:8-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
DB 24 NYGMN 28

RESULT 9  
S69305

hypothetical protein YLR280c - yeast (Saccharomyces cerevisiae)

N:Alternates names: hypothetical protein L8003.10-b

C:Species: Saccharomyces cerevisiae

C>Date: 20-Jul-1996 #sequence\_revision 23-Aug-1996 #text\_change 09-Jul-2004

C:Accession: S69305

R:Pauley, A.

submitted to the EMBL Data Library, November 1994

A:Description: The sequence of S. cerevisiae cosmid 8003.

A:Reference number: S50366

A:Accession: S69305

A:Molecule type: DNA

A:Residues: 1-116 <PAU>

A:Cross-references: UNIPROT:Q13541; EMBL:U17243; NID:G596030; PTDN:AA67350.1; PID:G2340

C:Gene: MIPS:YLR280c

A:Cross-references: SGD:S0004270

A:Map position: 12R

C:Superfamily: Saccharomyces hypothetical protein YLR280c

Query Match 100.0%; Score 30; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
DB 19 NYGMN 23

RESULT 10  
S19967

Ig heavy chain V region (M-T406) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S19967

R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mAb.

A:Reference number: S19963

A:Accession: S19967

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-118 <WEI>

A:Cross-references: UNIPROT:Q921A6; EMBL:X65090

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

P:12-95/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 118;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
DB 28 NYGMN 32

RESULT 11  
A53285

Ig heavy chain V and J regions, monoclonal antibody SCET.M8.1 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000

C:Accession: A53285

R:Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.

Mol. Immunol. 28, 1063-1072, 1991

A:Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struct

and their pH-reactivity profiles.

A:Reference number: A53285; MUID:92017897; PMID:1922102

A:Accession: A53285

A:Status: preliminary

A:Molecule type: DNA; protein

A:Residues: 1-119 <SAW>

A:Cross-references: GB:D12736; NID:G220595; PTDN:BA02228.1; PID:G220596

A>Note: sequence extracted from NCBI backbone (NCBIN:63271, NCBI:P:63299)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
DB 31 NYGMN 35

RESULT 12  
B42848

L6 mAb heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000

C:Accession: B42848; S33903

R:Well, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo,

J. Biol. Chem. 267, 15552-15558, 1992

A:Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and character

A:Reference number: A42848; MUID:92348410; PMID:1639794

A:Accession: B42848

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-120 <FEI>

A:Cross-references: GB:M90690; NID:G195065; PTDN:AAA38146.1; PID:G195066

A>Note: sequence extracted from NCBI backbone (NCBIN:109960, NCBI:P:109961)

A:Accession: S33903

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <FE2>

A:Cross-references: EMBL:M90691

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 120;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

DB 31 NYGMN 35

RESULT 13

S12953

Ig heavy chain V region (Y13-259) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999

C:Accession: S12953

R;Merge, T.M.; Biocca, S.; Cattaneo, A.

FEBS Lett. 274, 193-198, 1990

A>Title: Intracellular immunization. Cloning and intracellular expression of a monoclonal

A:Reference number: S12953; NUID:91071431; PMID:2123805

A:Accession: S12953

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-120 <MER>

A:Cross-references: GB:X55179; NID:G56471; PIDN:CAA38964.1; PID:G56472

A>Note: this sequence was determined from the germline gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 120;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

DB 31 NYGMN 35

RESULT 14

PH1404

Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jan-2000

C:Accession: PH1404; PH1406

R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; T

J. Exp. Med. 176, 1209-1214, 1992

A>Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in

la virus.

A:Reference number: PH1403; NUID:93018837; PMID:1402663

A:Accession: PH1404

A:Molecule type: DNA

A:Residues: 1-124 <SH1>

A:Accession: PH1406

A:Molecule type: DNA

A:Residues: 115-121 <SH2>

C:Genetics:

A:introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;35-118/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 124;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

DB 31 NYGMN 35

DB 51 NYGMN 55

RESULT 15  
S33905

Ig heavy chain precursor V region - synthetic

C:Species: synthetic

C>Date: 13-Jan-1995 #sequence\_revision 30-Apr-1998 #text\_change 20-Oct-2000

C:Accession: S33905

R;Li, A.Y.; Robinson, R.R.; Hellstroem, K.E.; Murray Jr., E.D.; Chang, C.P.; Hellstroem,

Proc. Natl. Acad. Sci. U.S.A. 84, 3439-3443, 1987

A>Title: Chimeric mouse-human IgG1 antibody that can mediate lysis of cancer cells.

A:Reference number: S33905; NUID:87204152; PMID:3106970

A:Accession: S33905

A:Molecule type: mRNA

A:Residues: 1-146 <LIU>

A:Cross-references: EMBL:M16072; NID:G195270; PIDN:AAA38229.1; PID:G195271

Query Match

Best Local Similarity 100.0%; Score 30; DB 4; Length 146;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

DB 50 NYGMN 54

Search completed: April 4, 2005, 15:58:00  
Job time : 2.80511 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 8.45048 Seconds  
(Without alignments)  
302.988 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_31\_35  
Perfect score: 30  
Sequence: 1 NYGMN 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	116	2	013541
2	30	100.0	175	1	HISS_BUCDN
3	30	100.0	226	1	Q73D74
4	30	100.0	244	2	Q65L51
5	30	100.0	261	2	Q6WDX4
6	30	100.0	299	2	Q924G6
7	30	100.0	300	2	Q6WDM3
8	30	100.0	301	2	Q6WDM2
9	30	100.0	302	2	Q924G5
10	30	100.0	305	2	Q895E8
11	30	100.0	316	2	Q9CLC4
12	30	100.0	323	2	Q8XS16
13	30	100.0	326	2	Q39726
14	30	100.0	326	2	Q85033
15	30	100.0	326	2	Q95379
16	30	100.0	332	2	Q814Y5
17	30	100.0	341	2	Q9N2S8
18	30	100.0	342	2	Q8XN57
19	30	100.0	387	2	Q6SHS8
20	30	100.0	398	2	Q97W83
21	30	100.0	422	2	Q7URZ8
22	30	100.0	423	2	Q975B4
23	30	100.0	479	2	Q7SBB0
24	30	100.0	725	2	Q6J3R6
25	30	100.0	726	2	Q66619
26	30	100.0	726	2	Q8ZHB0
27	30	100.0	729	2	Q8KR53
28	30	100.0	731	2	Q7UB05
29	30	100.0	731	2	Q6D8U6
30	30	100.0	732	1	IUTR_ECOLI
31	30	100.0	732	2	Q93PE2

32	30	100.0	732	2	Q6Q7N8	Q6Q7N8 escherichia
33	30	100.0	732	2	Q9XCH0	Q9XCH0 shigella fl
34	30	100.0	733	2	Q6KDX4	Q6KDX4 escherichia
35	30	100.0	733	2	Q6U607	Q6U607 klebsiella
36	30	100.0	759	2	Q83PM3	Q83PM3 shigella fl
37	30	100.0	759	2	Q8FDW0	Q8FDW0 escherichia
38	30	100.0	828	2	Q8SX93	Q8SX93 dirosophila
39	30	100.0	828	2	Q9VBYX0	Q9VBYX0 dirosophila
40	30	100.0	1119	2	Q815N6	Q815N6 plasmodium
41	30	100.0	1133	2	Q6CMR8	Q6CMR8 kluveromyc
42	30	100.0	1480	2	Q7RN37	Q7RN37 plasmodium
43	30	100.0	1959	2	Q8V3G5	Q8V3G5 swinepox vi
44	27	90.0	36	2	Q809B8	Q809B8 human rotav
45	27	90.0	36	2	Q809C3	Q809C3 human rotav

## ALIGNMENTS

RESULT 1	ID	013541	PRELIMINARY;	PRT;	116 AA.
AC	013541;				
DT	01-JAN-1998	(TREMBLrel. 05, Created)			
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)			
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)			
DE	Y1280CDP.				
GN	Name=Y1280CDP;				
OS	Saccharomyces cerevisiae (Baker's yeast).				
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.				
OX	NCBI_TaxID=4932;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97313267; PubMed=9169871;				
RA	Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansgorge W.,				
RA	Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,				
RA	Enrian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,				
RA	Heuss-Weitzel D., Hilbert H., Hilger F., Kline K., Kotter P.,				
RA	Louis B.J., Messenguy F., Mewes H.W., Mloaga T., Mostl D.,				
RA	Muller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,				
RA	Portetelle D., Purnelle B., Reckmann S., Rieger M., Rinke M., Rose M.,				
RA	Scharfe M., Scherens B., Scholler P., Schwaiger C., Schwarz P.,				
RA	Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhaesselt P.,				
RA	Vierendeels F., Voet M., Volckaert G., Voss H., Wandut R., Wedler E.,				
RA	Wedler H., Zimmermann F.K., Zollner A., Hant J., Holsel J.D.;				
RT	"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII. "				
RL	Nature 387:0-0(0).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Pauley A.;				
RA	Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Cherry J.M.;				
RA	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.				
DR	EMBL, U17243; AAB67350.1; -.				
DR	PIR, S69305; S69305.				
SQ	SEQUENCE 116 AA; 12951 MW; E31414157730E032 CRC64;				

Query Match 100.0%; Score 30; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 NYGMN 5
Db	19 NYGMN 23

```

RESULT 2
HIS5_BUCDN STANDARD; PRT; 175 AA.
ID Q84156;
AC 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP synthase subunit hisH) (IGP synthase subunit hisH) (IGP synthase subunit hisH) (IGP synthase subunit hisH) (Fragment).
GN Name=hisH;
OS Buchnera aphidicola (subsp. Diuraphis noxia).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
NCBI_TaxID=118101;
RN [1]
RP SEQUENCE FROM N.A.
RA Moran N.A., Mira A.;
RT "Levels of selection on genes of mutualistic endosymbionts.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IGP synthase catalyzes the conversion of PRFAR and glutamine to IGP, AICAR and glutamate. The hisH subunit provides the glutamine amidotransferase activity that produces the ammonia necessary to hisF for the synthesis of IGP and AICAR (By similarity).
CC -1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyxylulose-1-ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-aminoimidazole-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
CC -1- PATHWAY: Histidine biosynthesis; fifth step.
CC -1- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
-----
CC EMBL; AF465524; AAC33042.1; -.
DR HAMAP; MF_00278; -.1.
DR InterPro; IPR000991; GATase_1.
DR InterPro; IPR010139; IMP_synth_hisH.
DR Pfam; PF00117; GATase; 1.
DR TIGRPFAM; TIGR01855; IMP_synth_hisH; 1.
DR PROSITE; PS00442; GATASE_TYPE_I; 1.
KW Glutamine amidotransferase; Histidine biosynthesis; Transferase.
FT ACT_SITE 78 78 By similarity.
FT NON_TER 175 175
SQ SEQUENCE 175 AA; 19540 MW; E50851BA299D89C3 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 159 NYGMN 163

RESULT 3
Q73DT4 PRELIMINARY; PRT; 226 AA.
ID Q73DT4;
AC 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
GN Ordered locus names=BCE0627;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

```

```

OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Osekstad O.A., Helgeson E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolseae A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017266; AAS39561.1; -.
DR TIGR; BCE0627; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 226 AA; 25834 MW; 9CCB16555AD97185 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 218 NYGMN 222

RESULT 4
Q65L51 PRELIMINARY; PRT; 244 AA.
ID Q65L51;
AC Q65L51;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein (Peptidoglycan-binding LysoM).
DE LysM).
GN ORFNames=BL01953, BL401309;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 13;
RC PubMed=15383718;
RX Velth B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Weikl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an Organism with Great Industrial Potential.";
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.U.,
RA Tang W., de Leon A.L., Xiang H., Guetl V., Clausen I.G., Olsen P.B.,
RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA Berta R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; AE017333; AAU40213.1; -.
DR EMBL; CP000002; AAU22864.1; -.
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 25925 MW; 1561DF7670470E2 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 42 NYGMN 46

RESULT 5

```



```
OGWDM4
ID OGWDM4 PRELIMINARY; PRT; 261 AA.
AC OGWDM4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;
OS Acromys ignitus (flety spiny mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Acromys.
OX NCB1_TaxID=60745;
RN [1]
RP SEQUENCE FROM N.A.
RA Steppan S.J., Adkins R.M., Anderson J.;
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY294923; AA062681.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 261 261
SQ SEQUENCE 261 AA; 28136 MW; F3641198C9807A3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 261;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 185 NYGMN 189

RESULT 6
Q924G6 PRELIMINARY; PRT; 299 AA.
ID O924G6;
AC Q924G6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;
OS Meriones shawi (Shaw's jird).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCB1_TaxID=37435;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21219190; PubMed=11319262;
RA Adkins R.M., Galke E.L., Rowe D., Honeycutt R.L.;
RT "Molecular phylogeny and divergence time estimates for major rodent
RT groups: evidence from multiple genes.";
RL Mol. Biol. Evol. 18:777-791(2001).
DR EMBL; AF332021; AAK71897.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 299 299
SQ SEQUENCE 299 AA; 32452 MW; 5E624460D1D7243E CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 299;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 198 NYGMN 202

RESULT 7
Q6WDM3 PRELIMINARY; PRT; 300 AA.
ID Q6WDM3;
AC Q6WDM3;
```

```
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;
OS Beany's hindel (long-tailed pouched rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetomyinae;
OC Beany's.
OX NCB1_TaxID=70596;
RN [1]
RP SEQUENCE FROM N.A.
RA Steppan S.J., Adkins R.M., Anderson J.;
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY294904; AA062682.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 300 300
SQ SEQUENCE 300 AA; 32730 MW; 5211AC3F179BA984 CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 300;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 199 NYGMN 203

RESULT 8
Q6WDM2 PRELIMINARY; PRT; 301 AA.
ID Q6WDM2;
AC Q6WDM2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;
OS Cricetomys gambianus (Gambia rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetomyinae;
OC Cricetomys.
OX NCB1_TaxID=10085;
RN [1]
RP SEQUENCE FROM N.A.
RA Steppan S.J., Adkins R.M., Anderson J.;
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY294905; AA062663.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 301 301
SQ SEQUENCE 301 AA; 32706 MW; F599E104ECAF857D CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 301;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 200 NYGMN 204

RESULT 9
Q924G5 PRELIMINARY; PRT; 302 AA.
ID Q924G5;
AC Q924G5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;
```

```

OS Gerbillurus valliannus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Gerbillurus.
OX NCBI_TaxID=49440;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21219190; PubMed=11319262;
RA Atkins R.M., Geilke E.L., Rowe D., Honeycutt R.L.;
RT "Molecular phylogeny and divergence time estimates for major rodent
RT groups: evidence from multiple genes.";
RL Mol. Biol. Evol. 18:777-791(2001).
DR EMBL; AF332022; AAK71898.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 302 302
SQ SEQUENCE 302 AA; 32687 MW; C08D7478B24CEAC3 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 201 NYGMN 205

RESULT 10
Q895E8
ID Q895E8 PRELIMINARY; PRT; 305 AA.
AC Q895E8;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Hypoetical protein CTC01328.
GN OrderedlocusNames=CTC01328;
OS Clostridium tetani;
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Massachusetts / B88;
RX MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
RA Brueggemann H., Baumer S., Fricke W.F., Wiese A., Liesegang H.,
RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
RA Gottschalk G.;
RT "The genome sequence of Clostridium tetani, the causative agent of
RT tetanus disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
DR EMBL; AE015940; AAO35892.1; -.
KW Complete proteome.
SQ SEQUENCE 305 AA; 34802 MW; 6AEC3E38786B98D8 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 24 NYGMN 28

RESULT 11
Q9CLC4
ID Q9CLC4 PRELIMINARY; PRT; 316 AA.
AC Q9CLC4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CorA.
GN Name=CorA; OrderedlocusNames=PM1315;

```

```

OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006170; AAK03399.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015087; F:copal ion transporter activity; IEA.
DR GO; GO:0015095; F:magnesium ion transporter activity; IEA.
DR GO; GO:0006824; P:copal ion transport; IEA.
DR GO; GO:0015693; P:magnesium ion transport; IEA.
DR InterPro; IPR004488; CorA transp.
DR InterPro; IPR002523; Mg2+_transpCorA.
DR Pfam; PF01544; CorA; 1.
DR TIGRPFAM; TIGR00383; CorA; 1.
KW Complete proteome.
SQ SEQUENCE 316 AA; 36422 MW; AD3EFA4BC0ACC99 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 275 NYGMN 279

RESULT 12
Q8XS16
ID Q8XS16 PRELIMINARY; PRT; 323 AA.
AC Q8XS16;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE PROBABLE MAGNESIUM AND COBALT TRANSPORT TRANSMEMBRANE PROTEIN.
GN Name=RS01784; OrderedlocusNames=RS0665;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CM1100;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Guzy J., Mangenot S.,
RA Arlat M., Billault A., Broctier P., Camus J.C., Cattellico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunne S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Signier P., Thebault P., Whalen M., Winker P., Levy M.,
RA Weisenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646080; CAD17816.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0046873; F:metal ion transporter activity; IEA.
DR GO; GO:0030001; P:metal ion transport; IEA.
DR Pfam; PF01544; CorA; 1.
KW Complete proteome.
SQ SEQUENCE 323 AA; 36251 MW; DE264559E199DD61 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

```

Db 282 NYGMN 286

RESULT 13

ID 039726 PRELIMINARY; PRT; 326 AA.  
AC 039726;  
DT 01-JAN-1998 (TRENBLREL. 05, Created)  
DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)  
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
DE VP7.  
OS Human rotavirus G3.  
OC Viruses; deRNA viruses; Reoviridae; Rotavirus; Human rotavirus A.  
OX NCBI\_TaxID=73036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=97412814; PubMed=9267457;  
RA Wen L., Nakayama M., Yamashita Y., Nishio O., Fang Z.-Y., Nakagomi O.,  
RA Araki K., Nishimura S., Hasegawa A., Muller W.E., Ushijima H.;  
RL Arch. Virol. 142:1481-1489 (1997).  
RT "Genetic variation in the VP7 gene of human rotavirus serotype 3 (G3  
type) isolated in China and Japan."  
DR EMBL; D86274; BAA23294.1; -  
DR GO; GO:0019028; C:Viral capsid; IEA.  
DR InterPro; IPR001963; VP7.  
DR Pfam; PF00434; VP7; 1.  
DR ProDom; PD000191; VP7; 1.  
SQ SEQUENCE 326 AA; 37318 MW; ED2375A2CBA14234 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 326;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 52 NYGMN 56

RESULT 14

ID 085033 PRELIMINARY; PRT; 326 AA.  
AC 085033;  
DT 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)  
DE Outer capsid protein VP7.  
OS Porcine rotavirus.  
OC Viruses; deRNA viruses; Reoviridae; Rotavirus.  
OX NCBI\_TaxID=10913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Claret M., Luder J.E., Liprandi F.;  
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL; L35057; AAA47091.1; -  
DR GO; GO:0019028; C:Viral capsid; IEA.  
DR InterPro; IPR001963; VP7.  
DR Pfam; PF00434; VP7; 1.  
DR ProDom; PD000191; VP7; 1.  
SQ SEQUENCE 326 AA; 37078 MW; 36A21B861A8F8B3E CRC64;

Query Match 100.0%; Score 30; DB 2; Length 326;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 52 NYGMN 56

RESULT 15

ID 09E3T9 PRELIMINARY; PRT; 326 AA.  
AC 09E3T9;

DT 01-MAR-2001 (TRENBLREL. 16, Created)  
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)  
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)  
DE Outer capsid protein VP7.  
OS Human rotavirus A.  
OC Viruses; deRNA viruses; Reoviridae; Rotavirus.  
OX NCBI\_TaxID=10941;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=97/S48;  
RA Xu S., Wang J., Hung T.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF260957; AAG15360.1; -  
DR GO; GO:0019028; C:Viral capsid; IEA.  
DR InterPro; IPR001963; VP7.  
DR Pfam; PF00434; VP7; 1.  
DR ProDom; PD000191; VP7; 1.  
SQ SEQUENCE 326 AA; 37285 MW; 19479E95DAD21507 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 326;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 52 NYGMN 56

Search completed: April 4, 2005, 15:56:03  
Job time : 11.4505 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: April 4, 2005, 15:19:49 ; Search time 33.9457 Seconds  
(without alignments)  
193.690 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_50\_66  
Perfect score: 97  
Sequence: 1 WINTYTGSTYADDFKE 17

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneeqp1980s:\*  
2: geneeqp1990s:\*  
3: geneeqp2000s:\*  
4: geneeqp2001s:\*  
5: geneeqp2002s:\*  
6: geneeqp2003as:\*  
7: geneeqp2003bs:\*  
8: geneeqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	115	3	AA90823 520C9 hyb
2	97	100.0	243	2	AAW02280 520C9 ant
3	97	100.0	243	2	AAW53170 520C9 ant
4	97	100.0	243	2	AAW80424 520C9 gfv
5	97	100.0	243	7	ABW00716 520C9 gfv
6	97	100.0	246	2	AA39569 Sequence
7	97	100.0	267	4	AAU04944 Humanised
8	97	100.0	409	4	AAU04945 Humanised
9	97	100.0	534	2	AA39571 Sequence
10	89	91.8	253	3	AA828159 Murine an
11	89	91.8	365	2	AAW35131 R. pipien
12	89	91.8	366	2	AAW35132 R. pipien
13	87	89.7	183	1	AA70665 Sequence
14	87	89.7	183	1	AA82936 Variable
15	87	89.7	183	1	AA82938 Variable
16	87	89.7	183	1	AA82939 Variable
17	87	89.7	183	1	AA82939 Variable
18	87	89.7	183	1	AA82939 Variable
19	87	89.7	183	2	AAW10586 V region
20	87	89.7	183	2	AAW16341 L6 antiDo
21	87	89.7	183	2	AAW41068 Mouse L6
22	87	89.7	183	2	AAW47511 Mouse L6
23	87	89.7	183	2	AAW47518 Mouse L6
24	87	89.7	183	2	AAW89536 Anti-canc
25	87	89.7	183	4	AA898087 L6 VH CDN

26	87	89.7	183	7	ADC65008	ADC65008 Immunoglo
27	87	89.7	252	3	AA812562	AA812562 Chimeric
28	87	89.7	252	4	AA836825	AA836825 L6 gfv pr
29	85	87.6	230	2	AAW85695	AAW85695 Anti-IFN $\gamma$
30	85	87.6	235	2	AAW85694	AAW85694 Anti-IFN $\gamma$
31	85	87.6	240	2	AAW85693	AAW85693 Anti-IFN $\gamma$
32	85	87.6	267	2	AAW85688	AAW85688 Humanised
33	85	87.6	468	2	AAW85689	AAW85689 D9D10 bea
34	85	87.6	541	2	AAW85691	AAW85691 MoTabi an
35	85	87.6	711	2	AAW85692	AAW85692 MoTabi F
36	84	86.6	17	5	AAW85692	AAW85692 Anti-huma
37	84	86.6	17	8	AD87337	AD87337 Humanised
38	84	86.6	19	2	AAW17490	AAW17490 Mab 31.1
39	84	86.6	19	2	AAW06699	AAW06699 Human col
40	84	86.6	19	3	AAW83642	AAW83642 Biotin la
41	84	86.6	67	7	ADH62639	ADH62639 Mouse ant
42	84	86.6	70	7	ADH62638	ADH62638 Mouse ant
43	84	86.6	112	7	ADC27441	ADC27441 TMFFP2#18
44	84	86.6	112	7	ADC27449	ADC27449 TMFFP2#21
45	84	86.6	115	4	AA884740	AA884740 Variable

## ALIGNMENTS

RESULT 1  
AA90823 standard; protein, 115 AA.  
ID AA90823 standard; protein, 115 AA.  
AC AA90823; (first entry)  
XX 29-AUG-2000 (first entry)  
XX 520C9 hybridoma VH domain SEQ ID NO:24.  
DE 520C9 hybridoma VH domain SEQ ID NO:24.  
XX Antigen binding site; immunoglobulin; cancer antigen; immunological;  
XX antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;  
XX specific binding assay; affinity purification; drug targeting;  
XX toxin targeting; imaging; genetic; therapeutic.  
OS Homo sapiens.  
XX US6054561-A.  
XX 25-APR-2000.  
XX 07-JUN-1995; 95US-00483749.  
XX 08-FEB-1984; 84US-00577976.  
XX 11-JAN-1985; 85US-00690750.  
XX 21-MAR-1986; 86US-00842476.  
XX 08-MAY-1986; 88US-00190778.  
XX 11-AUG-1994; 94US-00288981.  
XX (CHTR ) CHIRON CORP.  
XX Ring DB;  
XX WPI; 2000-338508/29.  
XX N-PSDB; AAA38907.  
XX Monoclonal antibody capable of binding to human breast cancer antigen  
XX useful for affinity purification, drug or toxin targeting, imaging, and  
XX treating cancer.  
XX Disclosure; Fig 12; 57pp; English.  
XX The present invention describes a monoclonal antibody (Mab) (I) that  
XX binds to a human breast cancer antigen that is also bound by Mab 454C11  
XX and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also  
XX described is a hybridoma that produces (I). (I) is useful in specific  
XX binding assays, affinity purification, drug or toxin targeting, imaging,  
XX and genetic or immunological therapeutics for various cancers. The

CC Present sequence represents a VH domain derived from a 520C9 hybridoma,  
CC which is used in the exemplification of the present invention  
XX  
SQ Sequence 115 AA;

Query Match 100.0%; Score 97; DB 3; Length 115;  
Best Local Similarity 100.0%; Pred. No. 4.8e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFKE 17  
|||  
DB 50 WINTYTGSTYADDFKE 66

## RESULT 2

AAW02280  
ID AAW02280 standard; protein; 243 AA.

AC AAW02280;

XX 25-MAR-2003 (revised)

DT 29-OCT-1996 (first entry)

XX 520C9 anti-c-erbB-2 two single chain Fv construct.

XX 520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sfv;

KM construct; polypeptide linker; C-terminal amino acid sequence;

KM in vivo imaging; drug targeting experiment; homodimer; increased;

KM binding avidity; tissue retention time.

XX Homo sapiens.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 118..133  
/label= linker

XX US5534254-A.

XX 09-JUL-1996.

XX 07-OCT-1993; 93US-00133804.

XX 06-FEB-1992; 92US-00831967.

XX (CHIR ) CHIRON CORP.

PA (CREA-) CREATIVE BIOMOLECULES INC.

PI Oppermann H, Ring DB, Huston JS, Houston LL;

XX WPI; 1996-333194/73.

DR N-PSDB; AAT36880.

XX Compens. contg. antigen-targeting antibody fragment constructs -

FT comprising dimer of single-chain Fv fragments.

XX Example 1; Col 33-36; 30pp; English.

CC Variable heavy (VH) and variable light (VL) genes were cloned from a  
CC 520C9 hybridoma cDNA library, using probes directed toward the antibody  
CC constant and joining regions. A two single chain Fv (sfv) gene was  
CC constructed by connecting the VH and VL genes with a Ser rich polypeptide  
CC linker. The resulting 520C9 two sfv gene, which encodes the present  
CC sequence, was inserted into an expression vector, transformed into E.  
CC coli, and protein expression induced by the addn. of IPTG to the culture  
CC medium. A compsn. comprising a carrier and the 2 sfv protein prod. can be  
CC used for in vivo imaging, and drug targeting experiments. The 2 sfv  
CC protein prod. is a homodimer, in which both fragments target the same  
CC antigen, therefore giving greater binding avidity and longer tissue  
CC retention times, compared to individual sfv protein prod. fragments.  
CC (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 243 AA;

Query Match 100.0%; Score 97; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFKE 17  
|||  
DB 50 WINTYTGSTYADDFKE 66

## RESULT 3

AAW53170  
ID AAW53170 standard; protein; 243 AA.

AC AAW53170;

XX 16-JUL-1998 (first entry)

XX 520C9 anti-c-erbB-2 sfv' dimeric construct protein sequence.

KM Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer; c-erbB-2;

KM tumour; diagnosis; sg.

XX Synthetic.

OS Mus sp.

XX US5753204-A.

XX 19-MAY-1998.

XX 05-JUN-1995; 95US-00461838.

XX 06-FEB-1992; 92US-00831967.

XX 07-OCT-1993; 93US-00133804.

XX (CHIR ) CHIRON CORP.

PA (CREA-) CREATIVE BIOMOLECULES INC.

PI Oppermann H, Ring DB, Huston JS, Houston LL;

XX WPI; 1998-311318/27.

XX N-PSDB; AAV21798.

XX Imaging of antigens in vivo - using dimers of single-chain antibody Fv

FT fragments.

XX Example 1; Col 33-36; 30pp; English.

CC This represents the protein sequence of a 520C9 sfv' (single chain Fv)  
CC construct. This was constructed by connecting the VH and VL genes with a  
CC DNA sequence encoding a serine rich linker. 520C9 is a monoclonal  
CC antibody useful in targeting c-erbB-2 antigen. This dimeric construct can  
CC be used in the methods of invention of imaging a preselected antigen  
CC expressed in a mammal. The methods are used in magnetic resonance imaging  
CC of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic  
CC constructs have enhanced properties as in vivo targeting agents in  
CC comparison with intact monoclonal antibodies or their Fab fragments. The  
CC dimeric constructs permit the in vivo targeting of an epitope on an  
CC antigen with greater apparent avidity, including greater tumour  
CC specificity, tumour localisation and tumour retention properties than  
CC that of the Fab fragment having the same CDRs as the construct  
XX  
SQ Sequence 243 AA;

Query Match 100.0%; Score 97; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFKE 17  
|||  
DB 50 WINTYTGSTYADDFKE 66

## RESULT 4

AAW80424  
 ID AAW80424 standard; protein; 243 AA.  
 AC AAW80424;  
 XX  
 DT 28-JAN-1999 (first entry)  
 XX  
 DE 520C9 sFV sequence.  
 XX  
 KW 520C9 sFV; antigen; tumour cell; antibody 520C9; targeted delivery;  
 XX antigen-expressing cell.  
 XX  
 OS Synthetic.  
 XX  
 PN US5837846-A.  
 PD 17-NOV-1998.  
 XX  
 PF 05-JUN-1995; 95US-00461386.  
 XX  
 PR 06-FEB-1992; 92US-00831967.  
 XX  
 PR 07-OCT-1993; 93US-00133804.  
 XX  
 PA (CREA-) CREATIVE BIOMOLECULES INC.  
 PA (CHIR ) CHIRON CORP.  
 PI Oppermann H, Houston LL, Huston JS, Ring DB;  
 XX  
 XX WPI; 1999-023541/02.  
 DR N-PSDB; AAV63399.  
 XX  
 XX Nucleic acid encoding single-chain Fv fragment specific for antigens -  
 PT and having C-terminal tail for crosslinking to form dimer with improved  
 PT pharmacokinetic properties, used to deliver drugs and imaging agents,  
 especially to tumours.  
 XX  
 PS Example 1; Col 35-36; 29pp; English.  
 XX  
 CC The present sequence represents an antibody 520C9 sFV. Variable heavy and  
 CC light sequences of antibody 7520C9 are connected, together with a serine  
 CC linker, to produce the present single chain Fv gene. The present sequence  
 CC exemplifies the invention. Dimers of the single chain Fv are used for  
 CC targeted delivery of drugs or imaging agents (e.g. cytotoxins, produgs  
 CC or 9m-technetium) to antigen-expressing cells, particularly for  
 CC treatment or diagnosis of tumours (especially of ovary or breast)  
 CC  
 CC Sequence 243 AA;  
 SQ

Query Match 100.0%; Score 97; DB 2; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGOSTVADDFKE 17  
 DB 50 WINTYGOSTVADDFKE 66

RESULT 5  
 AAW00716  
 ID AAW00716 standard; protein; 243 AA.  
 AC AAW00716;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE 520C9 sFV protein.  
 XX  
 KW Cell proliferation; cytotoxic agent; drug targeting; single-chain Fv;  
 XX sFV.  
 XX Unidentified.  
 OS  
 XX  
 PN US2002168375-A1.

XX  
 PD 14-NOV-2002.  
 XX  
 PF 21-JUN-2001; 2001US-00887853.  
 XX  
 PR 06-FEB-1992; 92US-00831967.  
 XX  
 PR 07-OCT-1993; 93US-00133804.  
 PR 05-JUN-1995; 95US-00462641.  
 XX  
 PR 26-APR-2000; 2000US-00558741.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Huston JS, Houston LL, Ring DB, Oppermann H;  
 XX  
 XX WPI; 2003-765156/72.  
 DR N-PSDB; AAD61485.  
 XX  
 PT Novel binding protein formulation for targeting epitope on antigen in  
 PT mammal, comprising dimeric biosynthetic construct having conformation  
 PT permitting binding of antigen by binding site of each polypeptide chain.  
 XX  
 XX Example 1; Page 19-20; 30pp; English.  
 XX  
 CC The invention relates to a binding protein formulation for targeting an  
 CC epitope on an antigen expressed in mammal. The formulation comprises of  
 CC dimeric biosynthetic construct having conformation permitting binding of  
 CC antigen by binding site of each polypeptide chain. The invention is  
 CC useful for imaging a preselected antigen in a mammal expressing the  
 CC antigen. It is also useful for targeting drugs that inhibit cell  
 CC proliferation and cytotoxic agents that kill cells. The present sequence  
 CC is 520C9 sFV protein. This sequence is used in the exemplification of the  
 CC invention  
 CC  
 CC Sequence 243 AA;  
 SQ

Query Match 100.0%; Score 97; DB 7; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGOSTVADDFKE 17  
 DB 50 WINTYGOSTVADDFKE 66

RESULT 6  
 AAR39569  
 ID AAR39569 standard; protein; 246 AA.  
 XX  
 AC AAR39569;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-FEB-1994 (first entry)  
 XX  
 DE Sequence of 520C9 sFV protein.  
 XX  
 KW Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;  
 KW biosynthetic single polypeptide chain binding site; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9316185-A2.  
 PD 19-AUG-1993.  
 XX  
 PF 05-FEB-1993; 93WO-US001055.  
 XX  
 PR 06-FEB-1992; 92US-00831967.  
 XX  
 PA (CREA-) CREATIVE BIOMOLECULES INC.  
 PA (CETU ) CETUS ONCOLOGY CORP.  
 XX  
 PI Huston JS, Houston LL, Ring DB, Oppermann H;  
 XX

DR		MPI; 1993-272889/34.
DR	N-PeDB; AAQ46084.	
XX		
PT	New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for	
PT	imaging or treating breast or ovarian cancer etc.	
PS		
XX	Claim 4; Page 60-61; 87pp; English.	
CC	c-erbB-2 refers to a protein antigen expressed on the surface of tumour	
CC	cells, such as breast and ovarian tumour cells, which is an approx.	
CC	200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about	
CC	5.3 (see AAQ46083), AAR39568). A single chain Fv (scFv) is a covalently	
CC	linked VH-VL heterodimer which is expressed from a gene fusion including	
CC	VH- and VL- encoding genes connected by a peptide-encoding linker. Such	
CC	linker sequences are set forth in AA residues 116-135 in AAR39569, which	
CC	includes part of the 16 AA linker sequences in AAR39572. Using AAQ46084	
CC	for the 520C9 monoclonal antibody, a single chain polypeptide can be	
CC	produced having a binding affinity for a c-erbB-2 related antigen. 'X' in	
CC	AAR39569 refers to the location of a stop codon in AAQ46084. (Updated on	
CC	25-MAR-2003 to correct PN field.)	
SQ	Sequence 246 AA;	
Query Match	100.0%; Score 97; DB 2; Length 246;	
Best Local Similarity	100.0%; Pred. No. 1,1e-06;	
Matches 17; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 WINTYTGOSTYADDPKE 17                         	
Dd	50 WINTYTGOSTYADDPKE 66	
RESULT 7		
AAU04944		
XX	AAU04944 standard; protein; 267 AA.	
AC		
XX	AAU04944;	
DT	06-AUG-2003 (revised)	
DT	24-OCT-2001 (first entry)	
XX		
DE	Humanised anti-p185 single chain antibody, 520C9H.	
XX		
KW	Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunoconjugate;	
KM	cancer; tumour; adenocarcinoma.	
XX		
OS	Homo sapiens.	
OS	Mus sp.	
OS	Synthetic.	
OS	Chimeric.	
FH		
FH	Key	
FT	Region	
FT	/label= CDR	
FT	/note= "Complementarity determining region"	
FT	72..88	
FT	/label= CDR	
FT	/note= "Complementarity determining region"	
FT	138..152	
FT	/label= Synthetic peptide linker	
FT	/note= "Links the heavy chain to the light chain"	
FT	176..186	
FT	/label= CDR	
FT	/note= "Complementarity determining region"	
FT	202..208	
FT	/label= CDR	
FT	/note= "Complementarity determining region"	
FT	241..249	
FT	/label= CDR	
FT	/note= "Complementarity determining region"	
FT		

[illegible]



```

PT FT /label= CDR
PT FT /note= "Complementarity determining region"
PT FT 72. .88
PT FT /label= CDR
PT FT /note= "Complementarity determining region"
PT FT 121. .126
PT FT /label= CDR
PT FT /note= "Complementarity determining region"
PT FT Misc-difference 123
PT FT /note= "Encoded by GGG"
PT FT 138. .152
PT FT /label= Synthetic peptide linker
PT FT /note= "links the heavy chain to the light chain"
PT FT 176. .186
PT FT /label= CDR
PT FT /note= "Complementarity determining region"
PT FT 202. .208
PT FT /label= CDR
PT FT /note= "Complementarity determining region"
PT FT 241. .249
PT FT /label= CDR
PT FT /note= "Complementarity determining region"
PT FT Peptide 261. .276
PT FT /label= Synthetic linker peptide
PT FT /note= "links the antibody to the IL-2 molecule"
PT FT 277. .409
PT FT /label= IL_2
PT FT Misc-difference 406
PT FT /note= "Encode by ACA"
PT FT WO200153354-A2.
PT FT 26-JUL-2001.
PT FT 19-JAN-2001; 2001WO-US001919.
PT FT 20-JAN-2000; 2000US-0177258P.
PT FT (CHAR ) CHARON CORP.
PT FT (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.
PT FT (HAMI-) HAMILTON REGIONAL CANCER CENT.
PT FT Austin R, Kwok CS, Ring DB;
PT FT WPI; 2001-451904/48.
PT FT DR N-PSDB; AAS093508.
PT FT Novel immunconjugate useful for inhibiting tumor cell growth in vivo
PT FT comprises a humanized anti-p185 antibody linked to an Interleukin-2
PT FT polypeptide.
PT FT Claim 13; Fig 11; 74pp; English.
PT FT
PT FT The sequence represents a humanised anti-p185 (520C9) single chain
PT FT antibody/human interleukin-2 (IL-2) fusion protein. The fusion protein
PT FT (or immunconjugate) is used to inhibit the growth of tumours or cancers
PT FT particularly those characterised by overexpression of p185 e.g. human
PT FT adenocarcinomas and malignant and/or benign tumours of the breast, renal
PT FT system, salivary gland, gastrointestinal tract or gastric tumours.
PT FT (Updated on 06-AUG-2003 to correct OS field.)
PT FT
PT FT Sequence 409 AA;
PT FT
PT FT Query Match 100.0%; Score 97; DB 4; Length 409;
PT FT Best Local Similarity 100.0%; Pred. No. 1.9e-06;
PT FT Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PT FT
PT FT 1 WINTYGOSTYADDFKE 17
PT FT |||||
PT FT 72 WINTYGOSTYADDFKE 88
PT FT
PT FT RESULT 9

```

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AAR39571
ID AAR39571 standard; protein; 534 AA.
XX
AC AAR39571;
XX
DT 25-MAR-2003 (revised)
DT 07-FEB-1994 (first entry)
XX
DE Sequence of G-FIT.
XX
KW Tumour antigen; c-erbB-2; G-FIT.
XX
OS Synthetic.
XX
PN WO9316185-A2.
XX
PD 19-AUG-1993.
XX
PF 05-FEB-1993; 93WO-US001055.
XX
PR 06-FEB-1992; 92US-00831967.
XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
PA (CERTU ) CERTUS ONCOLOGY CORP.
XX
PI Huston JS, Houston LL, Ring DB, Oppermann H;
XX
XX WPI; 1993-272889/34.
XX DR N-PSDB; AAQ46086.
XX
PT New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for
PT imaging or treating breast or ovarian cancer etc.
XX
PS Example; Page 65-68; 87pp; English.
XX
CC c-erbB-2 refers to a protein antigen expressed on the surface of tumour
CC cells, such as breast and ovarian tumour cells, which is an approx.
CC 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about
CC 5.3 (see AAQ46083, AAR39568). (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 534 AA;
XX
XX
XX Query Match 100.0%; Score 97; DB 2; Length 534;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 WINTYGOSTYADDFKE 17
XX |||||
XX DB 339 WINTYGOSTYADDFKE 355
XX
XX RESULT 10
XX AAB28159
ID AAB28159 standard; protein; 253 AA.
XX
AC AAB28159;
XX
DT 08-FEB-2001 (first entry)
XX
DE Murine anti-BGP-2 single chain Fv fragment.
XX
KW Murine; immunoglobulin; antigen-binding; framework region; carcinoma;
KW c-erbB2; carcinoma-associated antigen.
XX
OS Mus sp.
XX
PN WO200061635-A2.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-EP003176.
XX
XX

```

PR 09-APR-1999; 99EP-00107030.  
 XX (UYZU-) UNIV ZUERICH.  
 PA (PLUE/) PLUECKTHUN A.  
 XX PI Plueckthun A, Honegger A, Willuda J;  
 XX WPI; 2000-679468/66.  
 DR Stabilizing chimeric immunoglobulin (Ig) involves setting up a stabilized  
 PT antigen binding Ig or its fragment by replacing one or more residues  
 PT present in acceptor Ig by those residues present in donor Ig.  
 PS Claim 6; Page 51; 51pp; English.  
 XX  
 XX The present invention relates to a method for stabilising a chimeric  
 CC immunoglobulin (Ig). The method comprises identifying antigen-binding  
 CC groups derived from donor Ig and framework regions derived from an  
 CC acceptor Ig. The present sequence is one such donor Ig fragment. One or  
 CC more of the residues present at the positions in the present sequence are  
 CC replaced by those present at the corresponding positions in the donor Ig,  
 CC after comparing the structural features of the VH domains of the acceptor  
 CC Ig and the donor Ig. The acceptor Ig fragment used in the present  
 CC invention is human anti-c-erbB2 single chain Fv fragment 4D5 (AA028158).  
 CC The method of the present invention is useful for producing a  
 CC pharmaceutical composition which can be used for treating human  
 CC carcinomas, since c-erbB2 is a carcinoma-associated antigen  
 XX  
 SQ Sequence 253 AA;  
 XX  
 Query Match 91.8%; Score 89; DB 3; Length 253;  
 Best Local Similarity 93.8%; Pred. No. 1.9e-05;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 WINTYTGSTYADDFK 16  
 DB 187 WINTYTGSTYADDFK 202  
 XX  
 RESULT 11  
 AAW35131  
 ID AAW35131 standard; protein; 365 AA.  
 XX  
 AC AAW35131;  
 XX  
 DT 20-APR-1998 (first entry)  
 XX  
 DE R. pipiens recombinant RNase ronc fusion protein 7.  
 XX  
 KW RNase A; ribonuclease; cytotoxic; onconase; ronc; immunofusion;  
 KW tumour cell growth; frog.  
 XX  
 OS Rana pipiens.  
 OS Synthetic.  
 OS  
 PN WO9731116-A2.  
 PD 28-AUG-1997.  
 PD  
 PF 19-FEB-1997; 97WO-US002588.  
 PF  
 PR 21-FEB-1996; 96US-0011800P.  
 PR  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 PI Rybak SM, Newton DL, Bogue L, Wlodawer A;  
 XX WPI; 1997-435168/40.  
 DR N-PSDB; AAT94969.  
 XX  
 PT Ribonuclease molecules based on native Onconase - used for killing cells,  
 PT particularly tumour cells.  
 XX

PS Disclosure; Page 73; 90pp; English.  
 XX  
 XX Sequences AAW35125 to AAW35135 represent recombinant fusion proteins  
 CC (ronc) which are modifications of the RNase Onconase (RTM) (ronc). Such  
 CC novel ribonuclease molecules are highly cytotoxic and can be used alone  
 CC or to form chemical conjugates or to target recombinant immunofusions.  
 CC They are used particularly for decreasing tumour cell growth. They can  
 CC also be used for cell separation in vitro by selectively killing unwanted  
 CC types of cells, e.g. in bone marrow prior to transplantation into a  
 CC patient undergoing marrow ablation by radiation, or for killing leukaemia  
 CC cells or T-cells that would cause graft versus host disease. The toxins  
 CC can also be used to selectively kill unwanted cells in culture. The new  
 CC ribonucleases have increased cytotoxic activity compared to ronc and also  
 CC lower immunogenicity in humans  
 XX  
 SQ Sequence 365 AA;  
 XX  
 Query Match 91.8%; Score 89; DB 2; Length 365;  
 Best Local Similarity 93.8%; Pred. No. 2.9e-05;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 WINTYTGSTYADDFK 16  
 DB 168 WINTYTGSTYADDFK 183  
 XX  
 RESULT 12  
 AAW35132  
 ID AAW35132 standard; protein; 366 AA.  
 XX  
 AC AAW35132;  
 XX  
 DT 20-APR-1998 (first entry)  
 XX  
 DE R. pipiens recombinant RNase ronc fusion protein 8.  
 XX  
 KW RNase A; ribonuclease; cytotoxic; onconase; ronc; immunofusion;  
 KW tumour cell growth; frog.  
 XX  
 OS Rana pipiens.  
 OS Synthetic.  
 OS  
 PN WO9731116-A2.  
 PD 28-AUG-1997.  
 PD  
 PF 19-FEB-1997; 97WO-US002588.  
 PF  
 PR 21-FEB-1996; 96US-0011800P.  
 PR  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 PI Rybak SM, Newton DL, Bogue L, Wlodawer A;  
 XX WPI; 1997-435168/40.  
 DR N-PSDB; AAT94970.  
 XX  
 PT Ribonuclease molecules based on native Onconase - used for killing cells,  
 PT particularly tumour cells.  
 XX  
 PS Disclosure; Page 74; 90pp; English.  
 XX  
 XX Sequences AAW35125 to AAW35135 represent recombinant fusion proteins  
 CC (ronc) which are modifications of the RNase Onconase (RTM) (ronc). Such  
 CC novel ribonuclease molecules are highly cytotoxic and can be used alone  
 CC or to form chemical conjugates or to target recombinant immunofusions.  
 CC They are used particularly for decreasing tumour cell growth. They can  
 CC also be used for cell separation in vitro by selectively killing unwanted  
 CC types of cells, e.g. in bone marrow prior to transplantation into a  
 CC patient undergoing marrow ablation by radiation, or for killing leukaemia  
 CC cells or T-cells that would cause graft versus host disease. The toxins  
 CC can also be used to selectively kill unwanted cells in culture. The new  
 CC ribonucleases have increased cytotoxic activity compared to ronc and also

```

CC      lower immunogenicity in humans
xx
xx      Sequence 366 AA;
SQ
Query Match          91.8%; Score 89; DB 2; length 366;
Beat Local Similarity 93.8%; Pred.No.2,9e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

Oy      1 WINTYTGOSTYADDPK 16
        |||||:|||||
Db      51 WINTYTGESTYADDPK 66

RESULT 13
AAP70625
AAP70625 standard; protein; 183 AA.
xx
xx      AAP70625;
AC
xx      03-OCT-2002 (revised)
DT
DT      09-APR-1991 (first entry)
xx
xx      Sequence encoded by the V region of the I6 VH CDNA clone p13-6a.
DE
xx      Chimeric antibody; Anti-cancer antibody.
KM
xx      Chimeric antibody; Anti-cancer antibody.
OS
xx      Mus sp.
FH
xx      Key
xx      Region
xx      Location/Qualifiers
xx      1..19
xx      /tag= a
xx      /label= leader peptide
xx      20..49
xx      /tag= b
xx      /label= FR1
xx      50..54
xx      /tag= c
xx      /label= CDR1
xx      55..68
xx      /tag= d
xx      /label= FR2
xx      69..85
xx      /tag= e
xx      /label= CDR2
xx      86..117
xx      /tag= f
xx      /label= FR3
xx      118..124
xx      /tag= g
xx      /label= CDR3
xx      125..139
xx      /tag= h
xx      /label= JH2
xx      129..139
xx      /tag= i
xx      /label= FR4
xx      140..183
xx      /tag= j
xx      /label= Cx2a

W08702671-A.
xx
xx      07-MAY-1987.
PD
xx
xx      27-OCT-1986; 86WO-US002269.
PF
xx      01-NOV-1985; 85US-00793980.
PR
xx      (ITGE-) INT GENETIC ENG INC.
PA
xx      (ROBI/) ROBINSON R R.
PI
xx      Robinson RR, Liu AY, Horwitz AH, Wall R;
xx

```

DR	WP1: 1987-136004/19.
DR	N-PSDB; AAN70969.
XX	
PT	Prodn. of immunoglobulin chains and molecules - is by recombinant DNA
PT	procedures, with chimeric antibodies etc. related to cancer specific
PT	antigens.
XX	
PS	Example; Fig 15; 126pp; English.
XX	
CC	The patentors claim a chimeric antibody molecule comprising 2 light
CC	chains and 2 heavy chains, each comprising a constant human region and a
CC	variable non-human region. Coding sequences for the Ig chains are also
CC	claimed. The invention provides consensus sequences of light and heavy
CC	chain J regions useful in the design of oligonucleotides (UTGs) for use
CC	as primers or probes for cloning immunoglobulinlight or heavy chain mRNAs
CC	or genes. Depending on the nature of design of a particular UIG, it may
CC	be capable of hybridizing to all Ig mRNAs or genes containing a single
CC	specific J sequence. UIG denotes universal immunoglobulin gene. (Updated
CC	on 03-OCT-2002 to add missing OS field.)
XX	
SQ	Sequence 183 AA;
Query Match	89.7%; Score 87; DB 1; Length 183;
Best Local Similarity	93.8%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0.	
QY	1 WINTYTGOSTYADDFK 16
Db	69 WINTYTGOPYADDFK 84
RESULT 14	
ID	AAP82936
XX	AAP82936 standard; protein; 183 AA.
XX	
AC	AAP82936;
XX	
DT	25-MAR-2003 (revised)
DT	03-OCT-2002 (revised)
DT	12-DEC-1990 (first entry)
XX	
DB	Variable region of the L6Vh cDNA clone pH3-6a.
XX	
XX	Mouse immunoglobulin; variable region; tumour antigen;
KW	chimeric antibodies; L6Vh; pH3-6a.
KX	
OS	Mus sp.
XX	
XX	
FH	Location/Qualifiers
FT	1..19
FT	/label= leader_peptide
FT	20..49
FT	/label= FR1
FT	50..54
FT	/label= CDR1
FT	55..68
FT	/label= FR2
FT	69..85
FT	/label= CDR2
FT	86..117
FT	/label= FR3
FT	118..128
FT	/label= CDR3
FT	125..139
FT	/label= Jh2
FT	129..183
FT	/label= FR4
FT	140..183
XX	/label= C gamma 2a
XX	
XX	W08803145-A.
XX	
XX	05-MAY-1988.
DD	

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XX PF 27-OCT-1987; 87WO-US002832.
XX PR 27-OCT-1986; 86US-00923244.
XX (ITGE-) INT GENETIC ENG INC.
XX (ONCO ) ONCOGEN.
XX (ONCO ) ONCOGEN.
XX Liu AY, Robinson RR, Hellstrom KE, Hellstrom I;
XX MPI: 1988-133226/19.
XX N-PSDB; AAN82417.
XX
XX PT New polynucleotide encoding variable region of mouse immunoglobulin -
XX specific for human tumour antigen, and expression products, including
XX complete chimeric human-mouse antibodies.
XX Disclosure; Page ?; 83pp; English.
XX
XX A library primed by oligo (dT) on L6 poly (A+) RNA was screened for kappa
XX clones with a mouse Ck region probe. From the L6 library, several clones
XX were isolated. A second screen with a 5' Jk5 specific probe identified
XX the L6 (Jk5) light-chain clones. Heavy chain clones of L6 were isolated
XX be screening with the JH2 oligonucleotide. The heavy and light chain
XX genes from the clones pH3-6a (and pL3-12a) were inserted into M13
XX bacteriophage vectors of which the sequence was determined by the
XX dideoxytermination method. Amino acid residues 26-35 have been confirmed
XX by peptide sequence. See also AAN82415-20. (Updated on 03-OCT-2002 to add
XX missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 183 AA;
SQ
XX
XX Query Match 89.7%; Score 87; DB 1; Length 183;
XX Best Local Similarity 93.8%; Pred. No. 2.8e-05;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WINTYTGOSTYADDFK 16
DB 69 WINTYTGQPTYADDFK 84
RESULT 15
ID AAP82938 standard; protein; 183 AA.
XX
XX AAP82938;
AC 25-MAR-2003 (revised)
XX 03-OCT-2002 (revised)
XX 12-DEC-1990 (first entry)
XX
XX Variable region of clone M13mp19-Cl-delta 4 (Cl-delta 4).
XX
XX Mouse immunoglobulin; variable region; tumour antigen;
XX chimeric antibodies; Bal-3i deletion clone M13mp19-Cl-delta 4.
XX
XX Mus sp.
XX
XX Location/Qualifiers
XX FH 1..19
XX FT /label= leader_peptide
XX FT 20..49
XX FT /label= FR1
XX FT 50..54
XX FT /label= CDR1
XX FT 55..68
XX FT /label= FR2
XX FT 69..85
XX FT /label= CDR2
XX FT 86..117
XX FT /label= FR3
XX FT 118..128
XX FT Region

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FT /label= CDR3
FT 125..139
FT /label= Jh2
FT 129..183
FT /label= FR4
FT 140..183
FT /label= C gamma 2a
PN WO8803145-A.
XX
XX PD 05-MAY-1988.
XX
XX PF 27-OCT-1987; 87WO-US002832.
XX
XX PR 27-OCT-1986; 86US-00923244.
XX
XX (ITGE-) INT GENETIC ENG INC.
XX (ONCO ) ONCOGEN.
XX (ONCO ) ONCOGEN.
XX Liu AY, Robinson RR, Hellstrom KE, Hellstrom I;
XX MPI: 1988-133226/19.
XX N-PSDB; AAN82419.
XX
XX PT New polynucleotide encoding variable region of mouse immunoglobulin -
XX specific for human tumour antigen, and expression products, including
XX complete chimeric human-mouse antibodies.
XX Disclosure; Page ?; 83pp; English.
XX
XX The nuclease Bal-3i was used to chew away the oligo (dC) in the L6 Vh
XX clone pH3-6a (AAN82417). For this clone nucleotides 1-38 were deleted.
XX Then the sequence was modified by site-directed mutagenesis with the M13
XX -ApaI primer. This 31-base primer introduces an ApaI site in the mouse Ch
XX gene at position at a position analogous to human Cgamma1 cDNA gene
XX module. See also AAN82415-20. (Updated on 03-OCT-2002 to add missing OS
XX field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 183 AA;
SQ
XX
XX Query Match 89.7%; Score 87; DB 1; Length 183;
XX Best Local Similarity 93.8%; Pred. No. 2.8e-05;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WINTYTGOSTYADDFK 16
DB 69 WINTYTGQPTYADDFK 84

```

Search completed: April 4, 2005, 15:47:08  
 Job time : 34.9457 secs

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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 25.0927 seconds

(without alignments)  
224.651 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_50\_66

Perfect score: 97

Sequence: 1 WINTYTGSTYADDFKE 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*

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16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	243	9	US-09-887-853-6
2	97	100.0	243	17	US-10-683-547-6
3	97	100.0	267	9	US-09-766-543-10
4	97	100.0	276	9	US-09-766-543-12
5	89	91.8	116	9	US-09-971-543-8
6	89	91.8	253	9	US-09-971-543-2
7	85	87.6	230	14	US-10-071-485-102
8	85	87.6	235	14	US-10-071-485-93
9	85	87.6	240	14	US-10-071-485-91
10	85	87.6	267	14	US-10-071-485-2
11	85	87.6	468	14	US-10-071-485-67
12	85	87.6	541	14	US-10-071-485-85
13	85	87.6	711	14	US-10-071-485-90

14	84	86.6	17	10	US-09-791-551-86	Sequence 86, App1
15	84	86.6	17	16	US-10-018-245A-2	Sequence 2, App1
16	84	86.6	17	16	US-10-467-253-5	Sequence 5, App1
17	84	86.6	67	14	US-10-243-130-19	Sequence 19, App1
18	84	86.6	70	14	US-10-243-130-17	Sequence 17, App1
19	84	86.6	70	14	US-10-243-130-18	Sequence 18, App1
20	84	86.6	70	17	US-10-901-650-17	Sequence 17, App1
21	84	86.6	70	17	US-10-901-650-18	Sequence 18, App1
22	84	86.6	70	17	US-10-901-650-19	Sequence 19, App1
23	84	86.6	112	15	US-10-383-447-10	Sequence 10, App1
24	84	86.6	112	15	US-10-383-447-18	Sequence 18, App1
25	84	86.6	116	14	US-10-138-727A-2	Sequence 2, App1
26	84	86.6	116	14	US-10-138-727A-18	Sequence 18, App1
27	84	86.6	116	14	US-10-138-727A-19	Sequence 19, App1
28	84	86.6	116	14	US-10-138-727A-20	Sequence 20, App1
29	84	86.6	116	14	US-10-138-727A-21	Sequence 21, App1
30	84	86.6	116	14	US-10-138-727A-22	Sequence 22, App1
31	84	86.6	116	14	US-10-138-727A-23	Sequence 23, App1
32	84	86.6	116	14	US-10-138-727A-24	Sequence 24, App1
33	84	86.6	116	14	US-10-138-727A-25	Sequence 25, App1
34	84	86.6	116	14	US-10-138-727A-26	Sequence 26, App1
35	84	86.6	116	14	US-10-310-719-30	Sequence 30, App1
36	84	86.6	116	14	US-10-310-719-33	Sequence 33, App1
37	84	86.6	116	15	US-10-468-370-658	Sequence 658, App
38	84	86.6	116	15	US-10-468-370-660	Sequence 660, App
39	84	86.6	116	15	US-10-468-370-662	Sequence 662, App
40	84	86.6	116	15	US-10-468-370-664	Sequence 664, App
41	84	86.6	116	15	US-10-468-370-666	Sequence 666, App
42	84	86.6	116	15	US-10-468-370-668	Sequence 668, App
43	84	86.6	116	15	US-10-468-370-670	Sequence 670, App
44	84	86.6	116	15	US-10-468-370-672	Sequence 672, App
45	84	86.6	116	16	US-10-468-496-2021	Sequence 2021, App

#### ALIGNMENTS

RESULT 1

US-09-887-853-6

/ Sequence 6, Application US/09887853

/ Patent No. US20020168375A1

/ GENERAL INFORMATION:

/ APPLICANT: Huston, James S.

/ Oppeermann, Hermann

/ Houston, L. L.

/ Ring, David B.

/ TITLE OF INVENTION: Biosynthetic Binding Proteins For

/ Imaging

/ NUMBER OF SEQUENCES: 11

/ CORRESPONDENCE ADDRESSES:

/ ADDRESS: Testa, Hurwitz & Thibault/Patent Department

/ STREET: Exchange Place, 53 State Street

/ CITY: Boston

/ STATE: Massachusetts

/ COUNTRY: USA

/ ZIP: 02109

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/887,853

/ FILING DATE: 21-Jun-2001

/ CLASSIFICATION: <Unknown>

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US/08/133,804

/ FILING DATE: <Unknown>

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Kelley, Robin D.

/ REGISTRATION NUMBER: 34,637

/ REFERENCE/DOCKET NUMBER: 2054/22

/ TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 243 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6
;
Query Match          100.0%; Score 97; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WINTYTGSTYADDFKE 17
DB      50 WINTYTGSTYADDFKE 66

RESULT 2
US-10-683-547-6
; Sequence 6, Application US/10683547
; Publication No. US20050058638A1
; GENERAL INFORMATION:
; APPLICANT: Houston, J.
; APPLICANT: Houston, L.L.
; APPLICANT: Ring, D.
; APPLICANT: Oppertmann, H.
; TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
; FILE REFERENCE: CIBT-P01-130
; CURRENT APPLICATION NUMBER: US/10/683,547
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/09/558,741
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 07/831,967
; PRIOR FILING DATE: 1992-02-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 520c9 sfv
US-10-683-547-6
;
Query Match          100.0%; Score 97; DB 17; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WINTYTGSTYADDFKE 17
DB      50 WINTYTGSTYADDFKE 66

RESULT 3
US-09-766-543-10
; Sequence 10, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: P01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
```

```

; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 520C9
; OTHER INFORMATION: humanized single-chain antibody used in the
; OTHER INFORMATION: IL-2-antibody fusions
US-09-766-543-10
;
Query Match          100.0%; Score 97; DB 9; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WINTYTGSTYADDFKE 17
DB      72 WINTYTGSTYADDFKE 88

RESULT 4
US-09-766-543-12
; Sequence 12, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: P01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: H520C9sfv plus
; OTHER INFORMATION: linker
US-09-766-543-12
;
Query Match          100.0%; Score 97; DB 9; Length 276;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WINTYTGSTYADDFKE 17
DB      72 WINTYTGSTYADDFKE 88

RESULT 5
US-09-971-543-8
; Sequence 8, Application US/09971543
; Patent No. US20020146846A1
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HONEGGER, ANNEMARIE
; APPLICANT: WILDUDA, JORG
; TITLE OF INVENTION: NOVEL METHOD FOR THE STABILIZATION OF CHIMERIC
; TITLE OF INVENTION: IMMUNOGLOBULINS OR IMMUNOGLOBULIN FRAGMENTS, AND
; TITLE OF INVENTION: STABILIZED ANTI-BGP-2 scfv FRAGMENT
; FILE REFERENCE: PLUCK-3 CON
; CURRENT APPLICATION NUMBER: US/09/971,543
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: PCT/EP00/03176
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: EP 99 10 7030.1
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
```

LENGTH: 116  
TYPE: PRT  
ORGANISM: Mus sp.  
US-09-971-543-8

Query Match  
Beet Local Similarity 91.8%; Score 89; DB 9; Length 116;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGSTYADDFK 16  
Db 50 WINTYGSTYADDFK 65

RESULT 6  
US-09-971-543-2  
Sequence 2, Application US/09971543  
Patent No. US20020146846A1  
GENERAL INFORMATION:

APPLICANT: PLUCKTHIN, ANDREAS  
APPLICANT: HONEGGER, ANNEMARIE  
APPLICANT: WILUDA, JORG  
TITLE OF INVENTION: NOVEL METHOD FOR THE STABILIZATION OF CHIMERIC  
TITLE OF INVENTION: IMMUNOGLOBULINS OR IMMUNOGLOBULIN FRAGMENTS, AND  
TITLE OF INVENTION: STABILIZED ANTI-EGF-2 scfv FRAGMENT

FILE REFERENCE: PLUCK-3 CON  
CURRENT APPLICATION NUMBER: US/09/971,543  
CURRENT FILING DATE: 2001-10-04  
PRIOR APPLICATION NUMBER: PCT/EP00/03176  
PRIOR FILING DATE: 2000-04-10  
PRIOR APPLICATION NUMBER: EP 99 10 7030.1  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2  
LENGTH: 253  
TYPE: PRT  
ORGANISM: Mus sp.  
US-09-971-543-2

Query Match  
Beet Local Similarity 91.8%; Score 89; DB 9; Length 253;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGSTYADDFK 16  
Db 187 WINTYGSTYADDFK 202

RESULT 7  
US-10-071-485-102  
Sequence 102, Application US/10071485  
Publication No. US2003009648A1  
GENERAL INFORMATION:

APPLICANT: Buyse, Marie-Ange  
APPLICANT: Sablon, Erwin  
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC  
TITLE OF INVENTION: SHOCK,  
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
FILE REFERENCE: INNS:015  
CURRENT APPLICATION NUMBER: US/10/071,485  
CURRENT FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: 09/485,737  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
PRIOR FILING DATE: 1998-08-14  
PRIOR APPLICATION NUMBER: EPO 98870139.7  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: EPO 97870122.5  
PRIOR FILING DATE: 1997-08-18  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 102

LENGTH: 230  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: SYNTHETIC  
US-10-071-485-102

Query Match  
Beet Local Similarity 87.6%; Score 85; DB 14; Length 230;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYGSTYADDFK 16  
Db 50 WINTYGSTYADDFK 65

RESULT 8  
US-10-071-485-93  
Sequence 93, Application US/10071485  
Publication No. US2003009648A1  
GENERAL INFORMATION:

APPLICANT: Buyse, Marie-Ange  
APPLICANT: Sablon, Erwin  
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC  
TITLE OF INVENTION: SHOCK,  
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
FILE REFERENCE: INNS:015  
CURRENT APPLICATION NUMBER: US/10/071,485  
CURRENT FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: 09/485,737  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
PRIOR FILING DATE: 1998-08-14  
PRIOR APPLICATION NUMBER: EPO 98870139.7  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: EPO 97870122.5  
PRIOR FILING DATE: 1997-08-18  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 93  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: SYNTHETIC  
US-10-071-485-93

Query Match  
Beet Local Similarity 87.5%; Score 85; DB 14; Length 235;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYGSTYADDFK 16  
Db 50 WINTYGSTYADDFK 65

RESULT 9  
US-10-071-485-91  
Sequence 91, Application US/10071485  
Publication No. US2003009648A1  
GENERAL INFORMATION:

APPLICANT: Buyse, Marie-Ange  
APPLICANT: Sablon, Erwin  
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC  
TITLE OF INVENTION: SHOCK,  
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
FILE REFERENCE: INNS:015  
CURRENT APPLICATION NUMBER: US/10/071,485  
CURRENT FILING DATE: 2002-02-07  
PRIOR APPLICATION NUMBER: 09/485,737  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
PRIOR FILING DATE: 1998-08-14

```

; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-91
```

```

Query Match      87.6%; Score 85; DB 14; Length 240;
Best Local Similarity 87.5%; Pred. No. 2,6e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYGQSTYADDFK 16
         |||||:|||||
Db      50 WINTYGESTYVDDFK 65
```

```

RESULT 10
US-10-071-485-2
; Sequence 2, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-071-485-2
```

```

Query Match      87.6%; Score 85; DB 14; Length 267;
Best Local Similarity 87.5%; Pred. No. 2,9e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYGQSTYADDFK 16
         |||||:|||||
Db      72 WINTYGESTYVDDFK 87
```

```

RESULT 11
US-10-071-485-67
; Sequence 67, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
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```

; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-67
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```

Query Match      87.6%; Score 85; DB 14; Length 468;
Best Local Similarity 87.5%; Pred. No. 5,1e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYGQSTYADDFK 16
         |||||:|||||
Db      70 WINTYGESTYVDDFK 85
```

```

RESULT 12
US-10-071-485-85
; Sequence 85, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-85
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```

Query Match      87.6%; Score 85; DB 14; Length 541;
Best Local Similarity 87.5%; Pred. No. 5,9e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYGQSTYADDFK 16
         |||||:|||||
Db      50 WINTYGESTYVDDFK 65
```

```

RESULT 13
US-10-071-485-90
; Sequence 90, Application US/10071485
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```
/ Publication No. US20030099648A1
/ GENERAL INFORMATION:
/ APPLICANT: Buyse, Marie-Ange
/ APPLICANT: Sablon, Edwin
/ TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
/ TITLE OF INVENTION: SHOCK,
/ TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
/ FILE REFERENCE: INNS:015
/ CURRENT APPLICATION NUMBER: US/10/071,485
/ PRIOR FILING DATE: 2002-02-07
/ PRIOR APPLICATION NUMBER: 09/485,737
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: PCT/EP 98/05165
/ PRIOR FILING DATE: 1998-08-14
/ PRIOR APPLICATION NUMBER: EPO 98870139.7
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: EPO 97870122.5
/ PRIOR FILING DATE: 1997-08-18
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 90
/ LENGTH: 711
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: SYNTHETIC
US-10-071-485-90
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Query Match      87.6%; Score 85; DB 14; Length 711;
Best Local Similarity 87.5%; Pred. No. 7.8e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 WINTYGOSTYADDFK 16
DB      70 WINTYGTSTYVDDFK 85
```

```
RESULT 14
US-09-791-551-86
/ Sequence 86, Application US/09791551
/ Publication No. US20030235584A1
/ GENERAL INFORMATION:
/ APPLICANT: KLOETZER, WILLIAM S.
/ APPLICANT: HANNA, NABIL
/ TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
/ FILE REFERENCE: 03/7003/0277869
/ CURRENT APPLICATION NUMBER: US/09/791,551
/ CURRENT FILING DATE: 2001-02-26
/ PRIOR APPLICATION NUMBER: 60/185,390
/ PRIOR FILING DATE: 2000-02-28
/ PRIOR APPLICATION NUMBER: 60/233,625
/ PRIOR FILING DATE: 2000-09-18
/ NUMBER OF SEQ ID NOS: 119
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 86
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Mus sp.
US-09-791-551-86
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```
Query Match      86.6%; Score 84; DB 10; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYGOSTYADDFK 16
DB      1 WINTYGTSTYVDDFK 16
```

```
RESULT 15
US-10-018-245A-2
/ Sequence 2, Application US/10018245A
/ Publication No. US20040115196A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: FUKUDA, Yoshiaki
/ APPLICANT: NAGAHIRA, Kazuhiro
/ APPLICANT: NAKANISHI, Toshihiro
/ TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement
/ TITLE OF INVENTION: determining regions and genes encoding the same
/ FILE REFERENCE: 46224
/ CURRENT APPLICATION NUMBER: US/10/018,245A
/ CURRENT FILING DATE: 2002-07-12
/ PRIOR APPLICATION NUMBER: JP 117394/2000
/ PRIOR FILING DATE: 2000-04-19
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: mouse
/ FEATURE:
/ OTHER INFORMATION: CDR-H2 of anti-human TNF-alpha antibody
US-10-018-245A-2
```

```
Query Match      86.6%; Score 84; DB 16; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYGOSTYADDFK 16
DB      1 WINTYGTSTYVDDFK 16
```

```
Search completed: April 4, 2005, 16:42:44
Job time : 26.0927 secs
```

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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:32:36 ; Search time 6.13738 Seconds

(without alignments)  
266.512 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_50\_66

Perfect score: 97

Sequence: 1 WINTYTGQSTYADDFKE 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

283416

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	89.7	115	2	SI9968
2	87	89.7	120	2	B42848
3	87	89.7	146	4	S33905
4	85	87.6	136	2	S35759
5	84	86.6	101	2	D24672
6	84	86.6	105	2	S24764
7	84	86.6	105	2	S24765
8	84	86.6	109	2	S26325
9	84	86.6	118	2	SI9967
10	84	86.6	119	2	A53285
11	84	86.6	124	2	PH1404
12	80	82.5	102	2	C32530
13	79	81.4	115	2	SI9965
14	76	78.4	114	2	D32967
15	76	78.4	114	2	C32967
16	76	78.4	117	2	S33187
17	76	78.4	117	2	S33190
18	75	77.3	105	2	S24766
19	75	77.3	113	2	B36259
20	74	76.3	118	2	A32530
21	74	76.3	119	2	S32530
22	71	73.2	118	2	S37204
23	70	72.2	120	2	SI9963
24	70	72.2	139	2	PH1225
25	69.5	71.6	119	2	H45722
26	69	69.1	114	2	PL0256
27	67	69.1	99	2	C24672
28	67	69.1	99	2	S26326
29	62	63.9	120	2	S26789

30	60	61.9	98	2	S46460	Ig heavy chain V r
31	57	58.8	134	2	S21916	Ig heavy chain V r
32	56	57.7	105	2	S24763	Ig heavy chain V r
33	55	56.7	98	2	A49051	Ig heavy chain V r
34	55	56.7	117	2	SI8554	Ig heavy chain V r
35	55	56.7	131	2	S26792	Ig heavy chain V r
36	54	55.7	446	2	S67437	Damage and replica
37	51	52.6	142	2	SI9245	Ig heavy chain pre
38	50	51.5	98	2	H34964	Ig heavy chain V-1
39	47	48.5	367	2	T26291	hypothetical prote
40	46	47.4	215	2	T27462	hypothetical prote
41	46	47.4	349	2	AF2130	iron(III) diclrat
42	45	46.4	122	2	PH0887	Ig heavy chain V r
43	45	46.4	125	2	E81192	hypothetical prote
44	45	46.4	209	2	AC0273	probable exported
45	44.5	45.9	324	2	A86839	conserved hypotet

#### ALIGNMENTS

##### RESULT 1

SI9968 Ig heavy chain V region (M-T408) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004

C/Accession: SI9968

R.Weissenhorn, W.; Riethmuller, G.; Weiser, E.M.; Rieber, E.P. submitted to the EMBL Data Library, March 1992

A/Description: Structural characterization of CD4 mAb.

A/Reference number: SI9963

A/Accession: SI9968

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-115 <WEI>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterodimer; immunoglobulin

F;10-93/Domain: immunoglobulin homology <IMM>

Query Match 89.7%; Score 87; DB 2; Length 115;  
Best Local Similarity 93.8%; Pred. No. 7.4e-07;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGQSTYADDFK 16  
DB 45 WINTYTGQSTYADDFK 60

##### RESULT 2

B42848 L6 mAb heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000

C/Accession: B42848; S33903

R.Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo, J. Biol. Chem. 267, 15552-15558, 1992

A/Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and character;

A/Reference number: A42848; MUID:92348410; PMID:1639794

A/Accession: B42848

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-120 <FEU>

A/Cross-references: GB:M90690; NID:9195065; PID:AAA38146.1; PID:9195066

A/Note: sequence extracted from NCBI backbone (NCBIN:109960, NCBIP:109961)

A/Accession: S33903

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-120 <FE2>

A/Cross-references: EMBL:M90691

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 89.7%; Score 87; DB 2; Length 120;  
Best Local Similarity 93.8%; Pred. No. 7.8e-07;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 50 WINTYTGQPTVADDFK 65

## RESULT 3

Ig heavy chain precursor V region - synthetic  
C/Species: synthetic  
C/Date: 13-Jan-1995 #sequence\_revision 30-Apr-1998 #text\_change 20-Oct-2000  
C/Accession: S33905  
R;Liu, A.Y.; Robinson, R.R.; Hellebroem, K.E.; Murray Jr., E.D.; Chang, C.P.; Hellebroem  
Proc. Natl. Acad. Sci. U.S.A. 84, 3439-3443, 1987  
A>Title: Chimeric mouse-human IgG1 antibody that can mediate lysis of cancer cells.  
A/Reference number: S33905; MUID:87204152; PMID:3306970  
A/Accession: S33905  
A/Molecule type: mRNA  
A/Residues: 1-146 <LIT>  
A/Cross-references: EMBL:MA6072; NID:G195270; PID:AAA38229.1; PID:G195271

Query Match 89.7%; Score 87; DB 4; Length 146;  
Best Local Similarity 93.8%; Pred. No. 9.6e-07;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGQSTYADDFK 16  
|||||:|||||  
Db 69 WINTYTGQPTVADDFK 84

## RESULT 4

BHBD10 protein - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C/Accession: S35759  
R;Froyen, G.F.V.  
submitted to the EMBL Data Library, May 1993  
A/Reference number: S35759  
A/Accession: S35759  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-136 <PRO>  
A/Cross-references: EMBL:X72796; NID:G312496; PID:CAA53316.1; PID:G312497  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
P;34-117/Domain: immunoglobulin homology <IMM>

Query Match 87.6%; Score 85; DB 2; Length 136;  
Best Local Similarity 87.5%; Pred. No. 1.9e-06;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGQSTYADDFK 16  
|||||:|||||  
Db 69 WINTYTGESTYVDDFK 84

## RESULT 5

Ig heavy chain V region (VGA3-8) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 23-Jul-1999  
C/Accession: D24672  
R;Winter, E.; Radbruch, A.; Krawinkel, U.  
EMBO J. 4, 2861-2867, 1985  
A/Reference number: A91022; MUID:86055722; PMID:2998759  
A/Accession: D24672  
A/Molecule type: DNA  
A/Residues: 1-101 <WIN>  
A/Cross-references: GB:X03301; NID:G51757; PIDN:CAA27040.1; PID:G773215  
A>Note: this sequence was determined from the differentiated gene

C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 86.6%; Score 84; DB 2; Length 101;  
Best Local Similarity 87.5%; Pred. No. 2e-06;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGQSTYADDFK 16  
|||||:|||||  
Db 31 WINTYTGEPYADDFK 46

## RESULT 6

Ig heavy chain V region (subgroup XI) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999  
C/Accession: S24764; S24772; S24777  
R;Klaeger, S.  
submitted to the EMBL Data Library, August 1992  
A/Reference number: S24763  
A/Accession: S24764  
A/Molecule type: DNA  
A/Residues: 1-105 <KLA>  
A/Cross-references: EMBL:Z14999  
A/Accession: S24772  
A/Molecule type: DNA  
A/Residues: 1-105 <KLW>  
A/Cross-references: EMBL:Z15011  
R;Thomas, J.W.  
submitted to the EMBL Data Library, August 1992  
A/Reference number: S24776  
A/Accession: S24777  
A/Molecule type: DNA  
A/Residues: 1-105 <THO>  
A/Cross-references: EMBL:Z15020; NID:G52616; PIDN:CAA78739.1; PID:G52617  
C/Genetics:  
A/Introns: 9/1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 86.6%; Score 84; DB 2; Length 105;  
Best Local Similarity 87.5%; Pred. No. 2.1e-06;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGQSTYADDFK 16  
|||||:|||||  
Db 62 WINTYTGEPYADDFK 77

## RESULT 7

Ig heavy chain V region (subgroup XI) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999  
C/Accession: S24765; S24773; S24778  
R;Klaeger, S.  
submitted to the EMBL Data Library, August 1992  
A/Reference number: S24763  
A/Accession: S24765  
A/Molecule type: DNA  
A/Residues: 1-105 <KLA>  
A/Cross-references: EMBL:Z15001  
A/Accession: S24773  
A/Molecule type: DNA  
A/Residues: 1-105 <KLW>  
A/Cross-references: EMBL:Z15013  
R;Thomas, J.W.  
submitted to the EMBL Data Library, August 1992  
A/Reference number: S24776  
A/Accession: S24778  
A/Molecule type: DNA  
A/Residues: 1-105 <THO>

A:Cross-references: EMBL:Z15022; NID:G52619; PIDN:CAA78741.1; PID:G52620

C:Genetics:

A:Introns: 9/1

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

Query Match 86.6%; Score 84; DB 2; Length 105;

Best Local Similarity 87.5%; Pred. No. 2.1e-06;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGSTVADDFK 16

Db 62 WINTYTGERTVADDFK 77

#### RESULT 8

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C:Accession: S26325

R:Stark, S.E.; Caton, A.U.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26325

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-109 <STA>

A:Cross-references: UNIPROT:Q921A6; EMBL:X59210; NID:G52080; PID:G1334043

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:5-88/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 84; DB 2; Length 109;

Best Local Similarity 87.5%; Pred. No. 2.1e-06;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGSTVADDFK 16

Db 40 WINTYTGERTVADDFK 55

#### RESULT 9

Ig heavy chain V region (M-T406) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S19967

R:Welschenborn, W.; Rietmuller, G.; Welts, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mAb.

A:Reference number: S19963

A:Accession: S19967

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-118 <WET>

A:Cross-references: UNIPROT:Q921A6; EMBL:X65090

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:12-95/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 84; DB 2; Length 118;

Best Local Similarity 87.5%; Pred. No. 2.3e-06;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGSTVADDFK 16

Db 47 WINTYTGERTVADDFK 62

#### RESULT 10

A53285

Ig heavy chain V and J regions, monoclonal antibody SCET.M8.1 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000

C:Accession: A53285

R:Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.

Mol. Immunol. 28, 1063-1072, 1991

A:Title: Molecular characterization of monoclonal anti-steroid antibodies: primary structure and their pH-reactivity profiles.

A:Reference number: A53285; MUID:92017897; PMID:1922102

A:Accession: A53285

A:Status: preliminary

A:Molecule type: DNA; protein

A:Residues: 1-119 <SAM>

A:Cross-references: GB:D12736; NID:9220595; PIDN:BA02228.1; PID:9220596

A>Note: sequence extracted from NCBI backbone (NCBIN:63271, NCBI:63299)

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 84; DB 2; Length 119;

Best Local Similarity 87.5%; Pred. No. 2.4e-06;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGSTVADDFK 16

Db 50 WINTYTGERTVADDFK 65

#### RESULT 11

Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jan-2000

C:Accession: PH1404; PH1406

R:Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Tai

J. Exp. Med. 176, 1209-1214, 1992

A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in t

la virus.

A:Reference number: PH1403; MUID:93018837; PMID:1402663

A:Accession: PH1404

A:Molecule type: DNA

A:Residues: 1-124 <SHI>

A:Accession: PH1406

A:Molecule type: DNA

A:Residues: 115-121 <SH2>

C:Genetics:

A:Introns: 16/1

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:35-118/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 84; DB 2; Length 124;

Best Local Similarity 87.5%; Pred. No. 2.5e-06;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGSTVADDFK 16

Db 70 WINTYTGERTVADDFK 85

#### RESULT 12

Ig heavy chain V region (10/8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 16-Aug-1996

C:Accession: C32530

R:Deverton, E.; Beret, C.; Tausel, M.; Feinstein, A.

Eur. J. Immunol. 17, 9-13, 1987

A:Title: Monoclonal BMB/c anti-progesterone antibodies use family IX variable region he

A:Reference number: A32530; MUID:87133855; PMID:3102254

A:Accession: C32530

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-102 <DEV>  
 A:Cross-References: GB:M27585  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 82.5%; Score 80; DB 2; Length 102;  
 Best Local Similarity 81.2%; Pred. No. 8.9e-06;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WINTYGQSTYADDFK 16  
 |||||:|||||  
 Db 33 WINTYGVPTTADDFK 48

## RESULT 13

S19965  
 Ig heavy chain V region (M-T321) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004  
 C:Accession: S19965

R:Weissenborn, W.; Riehmüller, G.; Weiss, E.M.; Rieber, E.P.  
 submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mAb.

A:Reference number: S19963

A:Accession: S19965

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-115 <WEI>

A:Cross-References: UNIPROT:Q921A6; EMBL:X65088

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 79; DB 2; Length 115;  
 Best Local Similarity 81.2%; Pred. No. 1.5e-05;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 WINTYGQSTYADDFK 16  
 |||||:|||||  
 Db 43 WINTYGVPTTADDFK 58

## RESULT 14

D32967  
 Ig heavy chain V region TE32 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 29-Jan-1990 #sequence\_revision 29-Jan-1990 #text\_change 21-Jan-2000

C:Accession: D32967

R:Levy, R.; Assulin, O.; Scherf, T.; Levitt, M.; Anglistter, J.

Biochemistry 28, 7168-7175, 1989

A:Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, prediction of amino acid sequences, prediction of amino acid sequences

A:Reference number: A32967; MUID:90057406; PMID:2819059

A:Accession: D32967

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-114 <LEV>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 76; DB 2; Length 114;  
 Best Local Similarity 81.2%; Pred. No. 4.4e-05;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WINTYGQSTYADDFK 16  
 |||||:|||||  
 Db 50 WINTYGVPTTADDFK 65

## RESULT 15

C32967

Ig heavy chain V region TE33 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 29-Jan-1990 #sequence\_revision 29-Jan-1990 #text\_change 21-Jan-2000  
 C:Accession: C32967  
 R:Levy, R.; Assulin, O.; Scherf, T.; Levitt, M.; Anglistter, J.  
 Biochemistry 28, 7168-7175, 1989  
 A:Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, prediction of amino acid sequences, prediction of amino acid sequences  
 A:Reference number: A32967; MUID:90057406; PMID:2819059  
 A:Accession: C32967  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-114 <LEV>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 76; DB 2; Length 114;  
 Best Local Similarity 81.2%; Pred. No. 4.4e-05;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WINTYGQSTYADDFK 16  
 |||||:|||||  
 Db 50 WINTYGVPTTADDFK 65

Search completed: April 4, 2005, 15:58:00  
 Job time : 6.13738 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 28.7316 Seconds  
(without alignments)  
302.988 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_50\_66  
Perfect score: 97  
Sequence: 1 WINTYTGSTYADDFKE 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	86.6	241	2	Q92IA6 mus musculus
2	75	77.3	102	2	Q9JL79 mus musculus
3	72	74.2	140	2	Q65EL3 mus sp. Egl
4	70	72.2	116	2	Q683Y7 mus musculus
5	68	70.1	116	2	Q683Y8 mus musculus
6	60	61.9	125	2	Q991A6 mus musculus
7	57	58.8	218	2	Q925S1 homo sapien
8	54	55.7	446	1	CRB3_SCHPO
9	53	54.6	745	2	Q6L2I9
10	51	52.6	759	2	Q8A3F1
11	48	49.5	2009	2	Q7N848
12	48	48.5	367	2	Q7YTW2
13	47	48.5	500	2	Q6N091
14	47	48.5	573	2	Q8A3Y7
15	46	47.4	2992	2	Q7RDX7
16	46	47.4	74	2	Q9A152
17	46	47.4	215	2	Q9NA29
18	46	47.4	349	2	Q8YTW6
19	46	47.4	357	2	Q6YOC2
20	46	47.4	576	2	Q65WZ7
21	46	47.4	2201	2	Q8GF46
22	45	46.4	125	2	Q9J517
23	45	46.4	209	1	RNFG_YERPE
24	45	46.4	209	2	Q65AG8
25	45	46.4	1085	2	Q85250
26	45	46.4	1235	2	Q7UD00
27	44.5	45.9	304	2	Q9N0Y0
28	44.5	45.9	324	2	Q9CEX1
29	44	45.4	612	2	Q9VTS5
30	44	45.4	617	2	Q7RE14
31	44	45.4	617	2	Q7RE14

32	44	45.4	793	2	Q6F9M7	Q6F9M7 acinetobact
33	44	45.4	1549	2	Q76D19	Q76D19 clostridium
34	44	45.4	2061	2	Q9YUH9	Q9YUH9 drosophila
35	44	45.4	2103	2	Q7KUL0	Q7KUL0 drosophila
36	43.5	44.8	434	2	Q913J2	Q913J2 pseudomonas
37	43.5	44.8	578	2	Q96V96	Q96V96 orpinomyces
38	43	44.3	173	2	Q959A8	Q959A8 galaxias vu
39	43	44.3	178	2	Q72W90	Q72W90 leprospira
40	43	44.3	178	2	Q8F9Y4	Q8F9Y4 leprospira
41	43	44.3	216	2	Q75H58	Q75H58 oryza sativ
42	43	44.3	216	2	Q87BA4	Q87BA4 xylella fas
43	43	44.3	218	2	Q9PEF0	Q9PEF0 xylella fas
44	43	44.3	329	2	Q8EJA4	Q8EJA4 shewanella
45	43	44.3	347	2	Q98D26	Q98D26 rhizobium 1

## ALIGNMENTS

```
RESULT 1
ID Q92IA6 PRELIMINARY; PRT; 241 AA.
AC Q92IA6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; Pubmed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; 1BMW.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 86.6%; Score 84; DB 2; Length 241;
Best Local Similarity 87.5%; Pred. No. 1,2e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFK 16
Db 50 WINTYTGSTYADDFK 65

RESULT 2
ID Q9JL79 PRELIMINARY; PRT; 102 AA.
AC Q9JL79;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

OX NCBI\_TaxID=10090;  
RN SEQUENCE FROM N.A.  
RC STRAIN=A.CA;  
RX MEDLINE=20448942; PubMed=10992488;  
RA DOI=10.1128/IAI.68.10.5803-5808.2000;  
RA Makiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "T-Cell-dependent antibody response to the dominant epitope of  
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
with cardiac myosin.";  
RL Infect. Immun. 68:5803-5808(2000).  
DR EMBL; AF26027; AAF69325.1; -.  
DR HSSP; P01751; INOB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG-LIKE; 1.  
FT NON\_TER 1  
FT SEQUENCE 102 AA; 11543 MW; ES90C292093F6711 CRC64;

Query Match 77.3%; Score 75; DB 2; Length 102;  
Best Local Similarity 81.2%; Pred. No. 0.00015;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 WINTYGGSTYADDFK 16  
Db 35 WINTETGPTVADDFK 50

## RESULT 3

ID 065ZL3 PRELIMINARY; PRT; 140 AA.  
AC 065ZL3;  
DT 25-OCT-2004 (TRENBLrel. 28, Created)  
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
GN Tg10H (Fragment).  
DR Name=Tg10H;  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9626537; PubMed=8699031; DOI=10.1016/0022-1759(96)00043-9;  
RA Noel D., Bernardi T., Navarro-Tenlon I., Martin M., Martinello J.P.,  
RA Ducancel F., Mani J.C., Pau B., Piechaczyk M., Biard-Piechaczyk M.;  
RT "Analysis of the individual contributions of immunoglobulin heavy and  
RT light chains to the binding of antigen using cell transfection and  
RT plasmon resonance analysis.";  
RL J. Immunol. Methods 193:177-187(1996).  
DR EMBL; S82492; AAB37434.2; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00409; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG-LIKE; 1.  
FT NON\_TER 140  
FT SEQUENCE 140 AA; 15302 MW; 7BF237F3D965F43 CRC64;

Query Match 74.2%; Score 72; DB 2; Length 140;  
Best Local Similarity 75.0%; Pred. No. 0.00068;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 WINTYGGSTYADDFK 16  
Db 69 WINTESGVPTVADDFK 84

## RESULT 4

0683Y7

ID 0683Y7 PRELIMINARY; PRT; 116 AA.  
AC 0683Y7;  
DT 25-OCT-2004 (TRENBLrel. 28, Created)  
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
DE Immunoglobulin heavy chain variable region (Fragment).  
GN Name=IGHV;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Balb/c;  
RA Phalipon A., Costachel C., Thuniz A., Nato F.;  
RT "Anti-lipopolysaccharide antibodies protective against Shigella  
RT flexneri 2a infection recognize an immunodominant serotype-specific  
RT determinant on the O-antigen.";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ784033; CAH04483.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PR00047; IGV; 1.  
DR SMART; SM00409; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG-LIKE; 1.  
FT NON\_TER 1  
FT SEQUENCE 116 AA; 12863 MW; 5EC1AD02E911952 CRC64;

Query Match 72.2%; Score 70; DB 2; Length 116;  
Best Local Similarity 75.0%; Pred. No. 0.0012;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 WINTYGGSTYADDFK 16  
Db 50 WINTETGPTVADDFK 65

## RESULT 5

ID 0683Y8 PRELIMINARY; PRT; 116 AA.  
AC 0683Y8;  
DT 25-OCT-2004 (TRENBLrel. 28, Created)  
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
DE Immunoglobulin heavy chain variable region (Fragment).  
GN Name=IGHV;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Balb/c;  
RA Phalipon A., Costachel C., Thuniz A., Nato F.;  
RT "Anti-lipopolysaccharide antibodies protective against Shigella  
RT flexneri 2a infection recognize an immunodominant serotype-specific  
RT determinant on the O-antigen.";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ784032; CAH04482.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00409; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG-LIKE; 1.  
FT NON\_TER 1  
FT SEQUENCE 116 AA; 12833 MW; C85932C0D843778D CRC64;

Query Match 72.2%; Score 70; DB 2; Length 116;



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OC      NCBI_TaxId=10090;
OX      [1]
RN      SEQUENCE FROM N A

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SEQUENCE FROM N.A

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RC STRAIN=BAJB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BAJB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL, AP240168; AAK43733.1; -.
DR HSSP, P01665; 1QNZ.
DR SMART, SM00406; IG, 1.
DR PROSITE, PS50835; IG, LIKE, 1.
FT NCN TER 218
FT SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;
SQ
Query Match 58.8%; Score 57; DB 2; Length 218;
Best Local Similarity 56.2%; Pred. No. 0.34;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Oy 1 WINTYTGQSTYADDFK 16
Db 52 WINTHSGVPKYAEFK 67
RESULT 9
CRB3_SCHPO STANDARD; PRT; 446 AA.
ID 010272;
AC 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE WD-repeat protein crb3.
GN Name=crb3; ORFNames=SPAC13G7.08c;
OS Schizosaccharomyces pombe (Pission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98070339; PubMed=9407031;
RA Saka Y., Ebashi F., Matsusaka T., Mochida S., Yanagida M.;
RT "Damage and replication checkpoint control in fission yeast is ensured
RT by interactions of Ctrp2, a protein with BRCT motif, with Cuts and
RT Chk1.";
RL Gene Dev. 11:387-3400(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown R., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmons M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welfens I., Vanstreels E., Rieger M., Schaefer M., Meller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Hoizer E., Moeser D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
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RA Eger P., Zimmermann W., Medler H., Wandut R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garçon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revela J.L., Moreno S., Armetrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Usero D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: Contains 5 WD repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC
DR EMBL, AB008572; BAA23358.1; -.
DR EMBL, Z69729; CAA93596.1; -.
DR PIR, T37658; S67437.
DR GeneDB, SPombe; SPAC13G7.08c; -.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011045; WD40_like.
DR Pfam; PF00400; WD40; 4.
DR PRINTS; PR00320; GPROTEINRPT.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 2.
KW Repeat; WD repeat.
FT REPEAT 74
FT REPEAT 113
FT REPEAT 74
FT REPEAT 113
FT REPEAT 155
FT REPEAT 172
FT REPEAT 214
FT REPEAT 216
FT REPEAT 257
FT REPEAT 294
FT REPEAT 333
FT REPEAT 455
SQ SEQUENCE 446 AA; 49506 MW; 4C42680926401A1 CRC64;
Query Match 55.7%; Score 54; DB 1; Length 446;
Best Local Similarity 52.9%; Pred. No. 2.3;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Oy 1 WINTYTGQSTYADDFKE 17
Db 243 WIPLYTGSTYPSNNVKE 259
RESULT 10
O6LZ19 PRELIMINARY; PRT; 745 AA.
ID O6LZ19;
AC O6LZ19;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein precursor.
GN OrderedLocustNames=MMP0638;
OS Methanococcus maripaludis.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=39152;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=52 / LL;
RA Hendrickson E.L., Kaul R., Zhou Y., Boyee D., Chapman P., Chung J.,
RA Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
RA Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
RA Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G.,
RA Saenphimachak C., Soli D., Whitman W.B., Larimer F.W., Olson M.V.,
RA Leigh J.A.;
RT "Complete genome sequence of the mesophilic hydrogenotrophic
RT methanogen Methanococcus maripaludis";
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RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX957220; CAF30194.1; -.
KW Complete proteome.
FT SIGNAL 1 22 Potential.
SQ SEQUENCE 745 AA; 84573 MW; 180855215DEE9953 CRC64;

Query Match
Best Local Similarity 54.6%; Score 53; DB 2; Length 745;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADD 14
DB 124 WVNYYGQSTYVID 137

RESULT 11
Q8A3F1 PRELIMINARY; PRT; 759 AA.
AC Q8A3F1;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BT3003;
OS Bacteroides thetaiotaomicron.
OC Bacteroidetes; Bacteroidales; Bacteroidia; Bacteroidaceae; Bacteroides.
OC NCBI_TaxID=819;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=1263928; DOI=10.1126/science.1080029;
RA Xu J., Bjurberg M.K., Hamrod J., Deng S., Carmichael L.K.,
  "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
  Science 299:2074-2076 (2003).
RL EMBL; AE016938; AA078109.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR001517; TIR.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 759 AA; 88928 MW; 52D975F32501538E CRC64;

Query Match
Best Local Similarity 52.6%; Score 51; DB 2; Length 759;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFK 16
DB 147 WINTFGRSNEIDFQ 162

RESULT 12
Q7N848 PRELIMINARY; PRT; 2009 AA.
AC Q7N848;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Similitates with peptide synthetase like pristinamycin I synthase
  3.
GN OrderedLocustNames=plu0899;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Photorhabdus.
OC NCBI_TaxID=141679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TT01;
RX MEDLINE=22957627; PubMed=14528314;

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RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
  Taourit S., Bocs S., Bouraux-Bude C., Chandler M., Charles J.-F.,
  Dassa E., Derose R., Derzelle S., Freysinet G., Gaudreau S.,
  RA Medigue C., Lenoir A., Powell K., Sigulier P., Vincent R., Wingate V.,
  RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
  RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
  luminescens.";
  Nat. Biotechnol. 21:1307-1313(2003).
CC -1- SIMILARITY: belongs to the ATP-dependent AMP-binding enzyme
  family.
DR EMBL; BX571861; CAE13194.1; -.
DR HSSP; P14687; IAMU.
DR Photolast; plu0899; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransferase; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR010071; AA adenyl_dom.
DR InterPro; IPR009081; ACP-like.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR001242; Condensatn.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR006163; Phosphopanteth_bind.
DR InterPro; IPR006162; Ppantne S.
DR InterPro; IPR000051; SAM bind.
DR Pfam; PF00501; AMP-binding; 1.
DR Pfam; PF00668; Condensation; 2.
DR Pfam; PF00550; PP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
DR PROSITE; PS00012; PHOSPHOPANTETHINE; 1.
KW Complete proteome; Phosphopantethine.
SQ SEQUENCE 2009 AA; 229657 MW; 82CD8C83D7813AC CRC64;

Query Match
Best Local Similarity 49.5%; Score 48; DB 2; Length 2009;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFKE 17
DB 1043 WINTYTBQPIALDQEE 1059

RESULT 13
Q7YTW2 PRELIMINARY; PRT; 367 AA.
AC Q7YTW2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein W08G11.1.
GN ORFNames=W08G11.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
  OC Rhabditidae; Pelodierinae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
  RT investigating biology.";
  Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Steward C.A.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z92817; CAB07296.1; -.
RX WormBase; WBGene00012346; W08G11.1.

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DR	MormPep; W08G11.1;	CEI6558.
DR	InterPro; IPR004951;	DUF266.
DR	Pfam; PF03269;	DUF268; 1.
KW	Hypothetical protein.	
SQ	SEQUENCE	367 AA; 42172 MW; F171013437F28509 CRC64;
Query Match	Similarity	48.5%; Score 47; DB 2; Length 367;
Best Local Matches	8; Conservative	53.3%; Pred. No. 28; Mismatches 3; Indels 4; Gaps 0;
OY	1 WINTYGCGSTYADDF	15 :: ::    330 WLDTYSGDSEAFDP 344

QY	DB	1	W	M	I	N	T	S	G	O	T	A	D	E	F	K	16	Score 47;	DB 2;	Length 500;	Pred. No. 38;	Mismatches 7;	Conservative 5;	Indels 4;	Gaps 0;
QY	DB	1	W	M	I	N	T	S	G	O	T	A	D	E	F	K	16	48.5%;	DB 2;	Length 500;	43.8%;	5;	Indels 4;	Gaps 0;	
DB		87	W	S	A	I	S	G	O	T	A	D	E	F	K	102									

RESULT 15		
ID	Q8A3Y7	PRELIMINARY; PRT; 573 AA.
AC	Q8A3Y7;	
DT	01-JUN-2003 (TREMblrel. 24, Created)	
DT	01-JUN-2003 (TREMblrel. 24, Last sequence update)	
DT	01-MAR-2004 (TREMblrel. 26, Last annotation update)	
DE	Putative TonB-dependent receptor.	
GN	OrderedLocusNames=BT2817;	
OS	Bacteroides thetaiotaomicron.	
OC	Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales; Bacteroidaceae; Bacteroides.	

OX NCBI\_TaxId=818;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STEIN=VPI-5482 / ATCC 29148;  
RX MEDLINE=22550858; PubMed=12639328; DOI=10.1126/science.1080029;  
RA Xu J., Blursell M.K., Hiarod J., Deng S., Carmichael L.K.,  
RA Chiang H.C., Hooper L.V., Gordon J.I.;  
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis." ,  
RL Science 299:2074-2076(2003) .  
DR EMBL; AEO16937; AA07923.1; "-  
DR GO: GO:0019867; C:outer membrane; IEA.  
DR GO: GO:0004872; F:receptor activity; IEA.  
DR GO: GO:0005215; F:transporter activity; IEA.  
DR GO: GO:0006810; P:transport; IEA.  
KW Complete proteome; Receptor.  
SQ SEQUENCE 573 AA; 64637 MW; 414CB2DCF2F14847 CRC64;

Query	March	48.5%	Score 47;	DB 2;	Length 573;
	Best local similarity	52.9%	Pred. No. 44;		
Matches	9;	Conservative	0;	Mismatches	8;
				Indels	0;
				Gaps	0;
QY	1	WINTYTGSTADDEKE	17		
Db	390	WINTYGYQDKADDFE	406		

Search completed: April 4, 2005, 15:56:06  
Job time : 31.7316 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:19:49 ; Search time 11.9808 seconds

(without alignments)  
193.690 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_99\_104

Perfect score: 34

Sequence: 1 RCFAY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq15Dec04:\*  
1: geneeqp19808:\*  
2: geneeqp19908:\*  
3: geneeqp20008:\*  
4: geneeqp20018:\*  
5: geneeqp20028:\*  
6: geneeqp20038:\*  
7: geneeqp20038:\*  
8: geneeqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	115	3	AA90823
2	34	100.0	227	2	AA06784
3	34	100.0	243	2	AAW02280
4	34	100.0	243	2	AAW53170
5	34	100.0	243	2	AAW80424
6	34	100.0	243	7	ABW00716
7	34	100.0	246	2	AA939569
8	34	100.0	267	2	AAU04944
9	34	100.0	453	6	ABU11979
10	34	100.0	534	2	AA939571
11	31	91.2	78	7	ADM26258
12	31	91.2	272	4	ABG05076
13	31	91.2	300	4	ABG17548
14	31	91.2	309	4	ABG14667
15	31	91.2	350	7	ADP59685
16	31	91.2	361	4	ABG04015
17	31	91.2	413	4	ABG21008
18	31	91.2	433	4	ABG07016
19	31	91.2	730	6	ABU21384
20	30	88.2	133	5	AAW48375
21	30	88.2	218	3	AAW74551
22	30	88.2	218	3	AAW74550
23	30	88.2	321	6	ABP77987
24	30	88.2	344	4	ABG18999
25	30	88.2	571	7	ABG79803

#### ALIGNMENTS

RESULT 1  
AA90823  
ID AA90823 standard; protein; 115 AA.  
XX  
AC AA90823;  
DT 29-AUG-2000 (first entry)  
XX  
DE 520C9 hybridoma VH domain SEQ ID NO:24.  
XX  
KW Antigen binding site; immunoglobulin; cancer antigen; immunological;  
KW antibody; tumour; human; mucin; cancer; cytotoxic; hybridoma;  
KW specific binding assay; affinity purification; drug targeting;  
KW toxin targeting; imaging; genetic; therapeutic.  
XX  
OS Homo sapiens.  
XX  
PN US6054561-A.  
XX  
PD 25-APR-2000.  
XX  
PF 07-JUN-1995; 95US-00483749.  
XX  
PR 08-FEB-1984; 84US-00577976.  
PR 11-JAN-1985; 85US-00690750.  
PR 21-MAR-1986; 86US-00842476.  
PR 08-MAY-1988; 88US-00190778.  
PR 11-AUG-1994; 94US-00288981.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
PI Ring DB;  
XX  
DR WPI; 2000-338508/29.  
DR N-PSDB; AAA38907.  
XX  
PT Monoclonal antibody capable of binding to human breast cancer antigen  
XX useful for affinity purification, drug or toxin targeting, imaging, and  
XX treating cancer.  
XX  
PS Disclosure; Fig 12; 57pp; English.  
XX  
CC The present invention describes a monoclonal antibody (Mab) (I) that  
CC binds to a human breast cancer antigen that is also bound by Mab 454C11  
CC and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also  
CC described is a hybridoma that produces (I). (I) is useful in specific  
CC binding assays, affinity purification, drug or toxin targeting, imaging,  
CC and genetic or immunological therapeutics for various cancers. The

CC present sequence represents a VH domain derived from a 520C9 hybridoma,  
 CC which is used in the exemplification of the present invention  
 XX  
 SQ Sequence 115 AA;

Query Match 100.0%; Score 34; DB 3; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RFGPAY 6  
 |||||  
 DB 99 RFGPAY 104

# RESULT 2

AAV06784 standard; protein; 227 AA.

AAV06784;

22-JUN-1999 (first entry)

M. grisea PTH3 gene product.

Fungal pathogenicity; imidazole glycerol phosphate dehydratase; PTH2;  
 carnitine acetyl transferase; membrane associated pathogenicity protein;  
 homeodomain transcription factor; PTH3, PTH11, PTH12.

Magnaporthe grisea.

MO9913094-A2.

18-MAR-1999.

08-SEP-1998; 98WO-US018730.

10-SEP-1997; 97US-0058460P.

(DUPO ) DU FONT DE NEMOURS & CO E. I.

Sveigard JA;

WPI; 1999-229247/19.

N-PSDB; AAX32293, AAX32294.

New isolated fungal pathogenicity genes.

Claim 15; Page 43-44; 50pp; English.

The invention relates to new isolated fungal pathogenicity genes,  
 designated PTH2, PTH3, PTH11 and PTH12 that are obtained from Magnaporthe  
 grisea. These novel genes encode proteins (AAV06783-86) that are highly  
 homologous to the fungal carnitine acetyl transferase enzyme, fungal  
 imidazole glycerol phosphate dehydratase enzyme, fungal membrane  
 associated pathogenicity protein or fungal homeodomain transcription  
 factor respectively. The novel genes are implicated in fungal  
 pathogenicity. Inhibition of any of the genes PTH2, PTH3, PTH11 and PTH12  
 results in the reduction or elimination of the pathogenic phenotype of  
 the fungus. The isolated genes are useful in the design of screens to  
 identify inhibitors of the fungal pathogenic gene products. The present  
 sequence represents the amino acid sequence of the PTH3 gene product  
 SQ Sequence 227 AA;

Query Match 100.0%; Score 34; DB 2; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RFGPAY 6  
 |||||  
 DB 118 RFGPAY 123

RESULT 3  
 AAM02280  
 ID AAM02280 standard; protein; 243 AA.  
 XX  
 AC AAM02280;

25-MAR-2003 (revised)  
 DT 29-OCT-1996 (first entry)

520C9 anti-c-erbB-2 two single chain Fv construct.

520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sfv;  
 construct; polypeptide linker; C-terminal amino acid sequence;  
 in vivo imaging; drug targeting experiment; homodimer; increased;  
 binding avidity; tissue retention time.

Homo sapiens.

Key Location/Qualifiers  
 Peptide 118..133  
 FT /label= linker

US5534254-A.

09-JUL-1996.

07-OCT-1993; 93US-00133804.

06-FEB-1992; 92US-00831967.

(CHTR ) CHIRON CORP.  
 (CREA-) CREATIVE BIOMOLECULES INC.

Oppermann H, Ring DB, Huston JS, Houston IL;

WPI; 1996-333194/33.

N-PSDB; AAT36880.

Compsns. contg. antigen-targeting antibody fragment constructs -  
 comprising dimer of single-chain Fv fragments.

Example 1; Col 33-36; 30pp; English.

Variable heavy (VH) and variable light (VL) genes were cloned from a  
 520C9 hybridoma cDNA library, using probes directed toward the antibody  
 constant and joining regions. A two single chain Fv (sfv) gene was  
 constructed by connecting the VH and VL genes with a Ser rich polypeptide  
 linker. The resulting 520C9 two sfv gene, which encodes the present  
 sequence, was inserted into an expression vector, transformed into E.  
 coli, and protein expression induced by the addn. of IPTG to the culture  
 medium. A compsn. comprising a carrier and the 2 sfv protein prod. can be  
 used for in vivo imaging, and drug targeting experiments. The 2 sfv  
 protein prod. is a homodimer, in which both fragments target the same  
 antigen, therefore giving greater binding avidity and longer tissue  
 retention times, compared to individual sfv protein prod. fragments.  
 (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 243 AA;

Query Match 100.0%; Score 34; DB 2; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 58;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RFGPAY 6  
 |||||  
 DB 99 RFGPAY 104

# RESULT 4

AAW53170  
 ID AAW53170 standard; protein; 243 AA.  
 XX  
 AC AAW53170;

AAW53170;

XX	DT	16-JUN-1998	(first entry)	
XX	DE	520C9 anti-c-erbB-2 sFv' dimeric construct protein sequence.		
XX	KW	Antigen imaging; single chain Fv; sFv; linker; dimeric; cancer; c-erbB-2;		
XX	KM	tumour; diagnosis; ss.		
XX	OS	Synthetic.		
XX	OS	Mus sp.		
XX	PN	US5753204-A.		
XX	PD	19-MAY-1998.		
XX	PF	05-JUN-1995; 95US-00461838.		
XX	PR	06-FEB-1992; 92US-00831967.		
XX	PR	07-OCT-1993; 93US-00133804.		
XX	PA	(CHIR ) CHIRON CORP.		
XX	PA	(CREA-) CREATIVE BIOMOLECULES INC.		
XX	PI	Oppermann H, Ring DB, Huston JS, Houston LL;		
XX	DR	WP1; 1998-311318/27.		
XX	DR	N-PSDB; AAV21798.		
XX	PT	Imaging of antigens in vivo - using dimers of single-chain antibody Fv		
XX	PT	fragments.		
XX	PS	Example 1, Col 33-36; 30pp; English.		
XX	CC	This represents the protein sequence of a 520C9 sFv' (single chain Fv)		
XX	CC	construct. This was constructed by connecting the Vh and Vl genes with a		
XX	CC	DNA sequence encoding a Serine rich linker. 520C9 is a monoclonal		
XX	CC	antibody useful in targeting c-erbB-2 antigen. This dimeric construct can		
XX	CC	be used in the methods of invention of imaging a preselected antigen		
XX	CC	expressed in a mammal. The methods are used in magnetic resonance imaging		
XX	CC	of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic		
XX	CC	constructs have enhanced properties as in vivo targeting agents in		
XX	CC	comparison with intact monoclonal antibodies or their Fab fragments. The		
XX	CC	dimeric constructs permit the in vivo targeting of an epitope on an		
XX	CC	antigen with greater apparent avidity, including greater tumour		
XX	CC	specificity, tumour localisation and tumour retention properties than		
XX	CC	that of the Fab fragment having the same CDRs as the construct		
XX	SO	Sequence 243 AA;		
XX	Query Match	100.0%; Score 34; DB 2; Length 243;		
XX	Best Local Similarity	100.0%; Pred. No. 58;		
XX	Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
XX	QY	1 RFGPAY 6		
XX				
XX	DB	99 RFGPAY 104		
XX	RESULT 5			
XX	AAW80424			
XX	AAW80424	standard; protein; 243 AA.		
XX	AAW80424;			
XX	AC			
XX	DT	28-JAN-1999 (first entry)		
XX	XX			
XX	DE	520C9 sFv sequence.		
XX	KW	520C9 sFv; antigen; tumour cell; antibody 520C9; targeted delivery;		
XX	KM	antigen-expressing cell.		
XX	XX			
XX	OS	Synthetic.		

```
PV      USS837846-A.
PD      17-NOV-1998.
PE      05-JUN-1995;    95US--00461386.
PX      06-FEB-1992;    92US--00831967.
PR      07-OCT-1993;    93US--00133804.
PV      (CREA-) CREATIVE BIOMOLECULES INC.
PA      (CHIR ) CHIRON CORP.
PI      Oppermann H, Houston LL, Huston JS, Ring DB;
        WPI, 1999-023541/02.
DR      N-PsDB; AAV63399.
PT      Nucleic acid encoding single-chain Fv fragment specific for antigens -
PR      and having C-terminal tail for crosslinking to form dimer with improved
PT      pharmacokinetic properties, used to deliver drugs and imaging agents,
PP      especially to tumours.
PX      Example 1; COL 35-36; 29pp; English.
PY      The present sequence represents an antibody 520C9 sFv. Variable heavy and
XX      light sequences of antibody 7520C9 are connected, together with a serine
CC      linker, to produce the present single chain Fv gene. The present sequence
CC      exemplifies the invention. Dimers of the single chain Fv are used for
CC      targeted delivery of drugs or imaging agents (e.g. cytotoxins, prodrugs
CC      or 9m+technetium) to antigen-expressing cells, particularly for
CC      treatment or diagnosis of tumours (especially of ovary or breast).
SQ      Sequence 243 AA;

Query Match          100.0%; Score 34; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 58;
Matches   6; Conservative    0; Mismatches     0; Indels    0; Gaps    0;

QY           1 RFGEAY 6         |||||
Db            99 RFGEAY 104       |

RESULT 6
ABM00716
ID ABM00716 standard; protein; 243 AA.
XX AC ABM00716;
XX AD
DT 15-JAN-2004 (first entry)
DE 520C9 sFv protein.
XX KW Cell proliferation; cytotoxic agent; drug targeting; single-chain Fv;
KW sFv.
XX OS Unidentified.
XX PN US2002168375-A1.
XX PD 14-NOV-2002.
XX PE 21-JUN-2001; 2001US--00887853.
XX PR 06-FEB-1992;    92US--00831967.
PR 07-OCT-1993;    93US--00133804.
PR 05-JUN-1995;    95US--00462641.
PR 26-APR-2000; 2000US--00558741.
XX PA (CHIR ) CHIRON CORP.
XX PI Huston JS, Houston JL, Ring DB, Oppermann H;
```

DR WPI: 2003-765156/72.  
DR N-PSDB; AAD61485.  
XX  
PT Novel binding protein formulation for targeting epitope on antigen in  
PT mammal, comprising dimeric biosynthetic construct having conformation  
PT permitting binding of antigen by binding site of each polypeptide chain.  
XX  
PS Example 1; Page 19-20; 30pp; English.  
XX  
CC The invention relates to a binding protein formulation for targeting an  
CC epitope on an antigen expressed in mammal. The formulation comprises of  
CC dimeric biosynthetic construct having conformation permitting binding of  
CC antigen by binding site of each polypeptide chain. The invention is  
CC useful for imaging a preslected antigen in a mammal expressing the  
CC antigen. It is also useful for targeting drugs that inhibits cell  
CC proliferation and cytotoxic agents that kill cells. The present sequence  
CC is 520C9 sfv protein. This sequence is used in the exemplification of the  
CC invention  
XX  
SQ Sequence 243 AA;  
XX  
Query Match 100.0%; Score 34; DB 7; Length 243;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RFGPAY 6  
Db 99 RFGPAY 104  
XX  
RESULT 7  
AAR39569  
ID AAR39569 standard; protein; 246 AA.  
XX  
AC AAR39569;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-FEB-1994 (first entry)  
XX  
DE Sequence of 520C9 sfv protein.  
XX  
KW Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;  
KW biosynthetic single polypeptide chain binding site; ss.  
XX  
OS Synthetic.  
XX  
PN WO9316185-A2.  
PD 19-AUG-1993.  
XX  
PF 05-FEB-1993; 93WO-US001055.  
XX  
PR 06-FEB-1992; 92US-00831967.  
XX  
PA (CREA-) CREATIVE BIOMOLECULES INC.  
PA (CETU) CETUS ONCOLOGY CORP.  
XX  
PI Huston JS, Houston LL, Ring DB, Oppermann H;  
XX  
DR WPI, 1993-272889/34.  
DR N-PSDB; AAQ46084.  
XX  
PT New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for  
PT imaging or treating breast or ovarian cancer etc.  
XX  
PS Claim 4; Page 60-61; 87pp; English.  
XX  
CC c-erbB-2 refers to a protein antigen expressed on the surface of tumour  
CC cells, such as breast and ovarian tumour cells, which is an approx.  
CC 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about  
CC 5.3 (see AAQ46083, AAR39568). A single chain Fv (sfv) is a covalently  
CC linked VH-VL heterodimer which is expressed from a gene fusion including  
CC VH- and VL- encoding genes connected by a peptide-encoding linker. Such

CC linker sequences are set forth in AA residues 116-135 in AAR39569, which  
CC includes part of the 16 AA linker sequences in AAR39572. Using AAQ46084  
CC for the 520C9 monoclonal antibody, a single chain polypeptide can be  
CC produced having a binding affinity for a c-erbB-2 related antigen. 'X' in  
CC AAR39569 refers to the location of a stop codon in AAQ46084. (Updated on  
CC 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 246 AA;  
XX  
Query Match 100.0%; Score 34; DB 2; Length 246;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RFGPAY 6  
Db 99 RFGPAY 104  
XX  
RESULT 8  
AAU04944  
ID AAU04944 standard; protein; 267 AA.  
XX  
AC AAU04944;  
XX  
DT 06-AUG-2003 (revised)  
DT 24-OCT-2001 (first entry)  
XX  
DE Humanised anti-p185 single chain antibody, 520C9H.  
XX  
KW Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunoconjugate;  
KW cancer; tumour; adenocarcinoma.  
XX  
OS Homo sapiens.  
OS Mus sp.  
OS Synthetic.  
OS Chimeric.  
XX  
FH Key Location/Qualifiers  
FT 53..57  
FT /label= CDR  
FT /note= "Complementarity determining region"  
FT 72..88  
FT /label= CDR  
FT /note= "Complementarity determining region"  
FT 121..126  
FT /label= CDR  
FT /note= "Complementarity determining region"  
FT 138..152  
FT /label= Synthetic peptide linker  
FT /note= "links the heavy chain to the light chain"  
FT 176..186  
FT /label= CDR  
FT /note= "Complementarity determining region"  
FT 202..208  
FT /label= CDR  
FT /note= "Complementarity determining region"  
FT 241..249  
FT /label= CDR  
FT /note= "Complementarity determining region"  
FT 260..267  
FT /label= G1u\_G1u\_epitope  
XX  
PN WO200153354-A2.  
XX  
PD 26-JUL-2001.  
XX  
PF 19-JAN-2001; 2001WO-US001919.  
XX  
PR 20-JAN-2000; 2000US-0177258P.  
XX  
PA (CHIR) CHIRON CORP.  
PA (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.  
PA (HAMI-) HAMILTON REGIONAL CANCER CENT.



```
XX Austin R, Kwok CS, Ring DB;
PI WPI; 2001-451904/48.
XX N-PSDB; AAS09507.
DR
XX Novel immunconjugate useful for inhibiting tumor cell growth in vivo
PT comprises a humanized anti-p185 antibody linked to an interleukin-2
PT polypeptide.
XX
XX Claim 7; Fig 9; 74pp; English.
PS
XX The sequence represents a humanised anti-p185 single chain antibody which
CC is linked to a human interleukin-2 (IL-2) molecule to make a fusion
CC protein. The fusion protein (or immunoconjugate) is used to inhibit the
CC growth of tumors or cancers particularly those characterised by
CC overexpression of p185 e.g. human adenocarcinomas and malignant and/or
CC benign tumors of the breast, renal system, salivary gland,
CC gastrointestinal tract or gastric tumours. (Updated on 06-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 267 AA;

Query Match          100.0%; Score 34; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6
DB 121 RFGPAY 126

RESULT 9
ABU11979
ID ABU11979 standard; protein; 453 AA.
XX
AC ABU11979;
XX
XX 23-OCT-2003 (revised)
DT 13-FEB-2003 (first entry)
XX
XX M. echinospora calicheamicin biosynthesis protein CalQ.
DE
XX Calicheamicin biosynthetic gene cluster; aryltetraaccharide; aglycone;
KM calicheamicin resistance; nonchromoprotein enediynes; enediynes resistance;
KM bone marrow cell; enzyme.
XX
XX Micromonospora echinospora; spp. calichensis.
OS
XX WO200279465-A2.
FN
XX 10-OCT-2002.
PD
XX 28-NOV-2001; 2001WO-US044285.
XX
XX 28-NOV-2000; 2000US-00724797.
FR
XX (SLOK ) SLOAN KETTERING INST CANCER RES.
PA
XX Thorson J;
XX
XX WPI; 2003-092897/08.
DR N-PSDB; AAX56041.
XX
XX Novel nucleic acid molecule from nonchromoprotein enediynes biosynthetic
PT gene cluster from Micromonospora echinospora useful for conferring
PT calicheamicin resistance on a subject.
XX
XX Claim 25; Page 107-108; 179pp; English.
PS
XX The present invention relates to the isolation of the Micromonospora
CC echinospora spp. calichensis calicheamicin biosynthetic gene cluster
CC encoding proteins and enzymes used in the biosynthetic production of
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```
CC calicheamicin, including aryltetraaccharide and aglycone. The gene
CC cluster also includes the gene encoding for the protein that confers
CC calicheamicin resistance. The calicheamicin biosynthetic gene cluster is
CC a nonchromoprotein enediynes biosynthetic gene cluster. Expression vectors
CC containing genes from the biosynthetic gene cluster are also disclosed.
CC The expression vectors are useful for producing calicheamicin
CC biosynthetic proteins. The calicheamicin self-resistance gene provides an
CC approach for gene therapy, for example, by introduction of enediynes
CC resistance genes into bone marrow cells, thus increasing resistance and
CC allowing tolerance to chemotherapeutic doses of calicheamicin. ABU11964-
CC ABU12010 represent proteins and enzymes encoded by genes in the M.
CC echinospora calicheamicin biosynthesis gene cluster. (Updated on 23-OCT-
CC 2003 to standardise OS field)
XX
SQ Sequence 453 AA;

Query Match          100.0%; Score 34; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6
DB 443 RFGPAY 448

RESULT 10
AAR39571
ID AAR39571 standard; protein; 534 AA.
XX
AC AAR39571;
XX
XX 25-MAR-2003 (revised)
DT 07-FEB-1994 (first entry)
XX
XX Sequence of G-FIT.
DE
XX Tumour antigen; C-erbB-2; G-FIT.
XX
XX Synthetic.
OS
XX WO9316185-A2.
XX
XX 19-AUG-1993.
PD
XX 05-FEB-1993; 93WO-US001055.
XX
XX 06-FEB-1992; 92US-00831967.
XX
XX (CREA-) CREATIVE BIOMOLECULES INC.
PA (CETU ) CETUS ONCOLOGY CORP.
XX
XX Huston JS, Houston LL, Ring DB, Oppermann H;
PI
XX WPI: 1993-272889/34.
DR N-PSDB; AAQ46086.
XX
XX New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for
PT imaging or treating breast or ovarian cancer etc.
PT
XX Example; Page 65-68; 87pp; English.
PS
XX C-erbB-2 refers to a protein antigen expressed on the surface of tumour
CC cells, such as breast and ovarian tumour cells, which is an approx.
CC 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about
CC 5.3 (see AAQ46083, AAR3568). (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 534 AA;

Query Match          100.0%; Score 34; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 RRGFAY 6  
|||||  
XX 388 RRGFAY 393

RESULT 11  
ADM26258  
ID ADM26258 standard; protein; 78 AA.

XX ADM26258;

XX 20-MAY-2004 (first entry)

DE Hyperthermophile Methanopyrus kandleri protein #864.

KW hyperthermophile; protein stability enhancement;

KM protein activity enhancement.

XX Methanopyrus kandleri.

XX WO2003076575-A2.

XX 18-SEP-2003.

XX 04-MAR-2003; 2003WO-US006664.

XX 04-MAR-2002; 2002US-0361742P.

XX 14-MAY-2002; 2002US-0380423P.

XX 16-SEP-2002; 2002US-0410974P.

XX (FIDE-) FIDELITY SYSTEMS INC.

XX (MALY-) MALYKH A.

XX Slesarev AI, Pavlov A, Pavlova N, Kozyaevkin S;

XX WPI; 2003-748363/70.

XX N-PSDB; ADM27081.

PT New isolated nucleic acids encoding any of about 1700 Methanopyrus

PT kandleri proteins, and the encoded proteins, useful as medicaments or

PT as diagnostic agents.

XX Claim 31; SEQ ID NO 864; 1023bp; English.

XX The invention comprises the amino acid sequence of proteins from the

XX hyperthermophile Methanopyrus kandleri, the invention also comprises the

XX complete genome from Methanopyrus kandleri. The Methanopyrus kandleri

XX proteins of the invention are useful for enhancing the stability and/or

XX activity of other proteins. The Methanopyrus kandleri genome is useful in

XX a variety of diagnostic and analytical methods. The present amino acid

XX sequence represents a Methanopyrus kandleri protein of the invention.

OY 1 RRGFAY 6  
:|||||  
Db 40 KRGFAY 45

RESULT 12

ABG05076  
ID ABG05076 standard; protein; 272 AA.

XX ABG05076;

XX 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #5067.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KM food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS69263.

XX Claim 20; SEQ ID NO 35435; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

XX sequences. (I) is useful as hybridisation probes, polymerase chain

XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

XX and in recombinant production of (II). The polynucleotides are also used

XX in diagnostics as expressed sequence tags for identifying expressed

XX genes. (II) is useful in gene therapy techniques to restore normal

XX activity of (II) or to treat disease states involving (II). (II) is

XX useful for generating antibodies against it, detecting or quantitating a

XX polypeptide in tissue, as molecular weight markers and as a food

XX supplement. (II) and its binding partners are useful in medical disorders

XX of sites expressing (II). (I) and (II) are useful for treating disorders

XX involving aberrant protein expression or biological activity. The

XX polypeptide and polynucleotide sequences have applications in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits to assess biodiversity

XX and to produce other types of data and products dependent on DNA and

XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

XX patent did not appear in the printed specification, but was obtained in

XX electronic format directly from WIPO at

XX ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 272 AA;

XX Query Match 91.2%; Score 31; DB 4; Length 272;

XX Best Local Similarity 83.3%; Pred. No. 2.6e+02;

XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX OS Homo sapiens.  
XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US008631.  
XX PR 31-MAR-2000; 2000US-00540217.  
XX PR 23-AUG-2000; 2000US-00649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Dmanac RT, Liu C, Tang YT;  
XX WPI: 2001-639362/73.  
XX DR N-PSDB; AAS81735.  
XX PT New isolated polynucleotide and encoded polypeptides, useful in  
XX PT diagnostics, forensics, gene mapping, identification of mutations  
XX PT responsible for genetic disorders or other traits and to assess  
XX PT biodiversity.  
XX PS Claim 20; SEQ ID NO 47907; 103pp; English.  
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain  
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
XX CC and in recombinant production of (II). The polynucleotides are also used  
XX CC in diagnostics as expressed sequence tags for identifying expressed  
XX CC genes. (I) is useful in gene therapy techniques to restore normal  
XX CC activity of (II) or to treat disease states involving (II). (II) is  
XX CC useful for generating antibodies against it, detecting or quantitating a  
XX CC polypeptide in tissue, as molecular weight markers and as a food  
XX CC supplement. (II) and its binding partners are useful in medical imaging  
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders  
XX CC involving aberrant protein expression or biological activity. The  
XX CC polypeptide and polynucleotide sequences have applications in  
XX CC diagnostics, forensics, gene mapping, identification of mutations  
XX CC responsible for genetic disorders or other traits to assess biodiversity  
XX CC and to produce other types of data and products dependent on DNA and  
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
XX CC amino acid sequences of the invention. Note: The sequence data for this  
XX CC patent did not appear in the printed specification, but was obtained in  
XX CC electronic format directly from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 300 AA;  
OY Query Match 91.2%; Score 31; DB 4; Length 300;  
Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 1 RFGPAY 6  
273 RYGFAY 278  
RESULT 14  
ID ABG14667 standard; protein; 309 AA.  
AC ABG14667;  
XX 18-FEB-2002 (first entry)  
XX DE Novel human diagnostic protein #14658.  
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX OS Homo sapiens.

XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US008631.  
XX PR 31-MAR-2000; 2000US-00540217.  
XX PR 23-AUG-2000; 2000US-00649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Dmanac RT, Liu C, Tang YT;  
XX WPI: 2001-639362/73.  
XX DR N-PSDB; AAS78854.  
XX PT New isolated polynucleotide and encoded polypeptides, useful in  
XX PT diagnostics, forensics, gene mapping, identification of mutations  
XX PT responsible for genetic disorders or other traits and to assess  
XX PT biodiversity.  
XX PS Claim 20; SEQ ID NO 45026; 103pp; English.  
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain  
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
XX CC and in recombinant production of (II). The polynucleotides are also used  
XX CC in diagnostics as expressed sequence tags for identifying expressed  
XX CC genes. (I) is useful in gene therapy techniques to restore normal  
XX CC activity of (II) or to treat disease states involving (II). (II) is  
XX CC useful for generating antibodies against it, detecting or quantitating a  
XX CC polypeptide in tissue, as molecular weight markers and as a food  
XX CC supplement. (II) and its binding partners are useful in medical imaging  
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders  
XX CC involving aberrant protein expression or biological activity. The  
XX CC polypeptide and polynucleotide sequences have applications in  
XX CC diagnostics, forensics, gene mapping, identification of mutations  
XX CC responsible for genetic disorders or other traits to assess biodiversity  
XX CC and to produce other types of data and products dependent on DNA and  
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
XX CC amino acid sequences of the invention. Note: The sequence data for this  
XX CC patent did not appear in the printed specification, but was obtained in  
XX CC electronic format directly from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 309 AA;  
OY Query Match 91.2%; Score 31; DB 4; Length 309;  
Best Local Similarity 83.3%; Pred. No. 3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 1 RFGPAY 6  
215 RYGFAY 220  
RESULT 15  
ID ADF59685 standard; protein; 350 AA.  
AC ADF59685;  
XX 12-FEB-2004 (first entry)  
XX DE Human polypeptide sequence SEQ ID NO:2052.  
XX KW biological activity; genetic engineering; hybridisation probe; oligomer;  
XX KW primer; chromosome mapping; gene mapping; recombinant protein production;  
XX KW human.  
XX OS Homo sapiens.

FN WO2003080795-A2.

XX 02-OCT-2003.

PD 09-AUG-2002; 2002WO-US025485.

XX 09-AUG-2001; 2001US-0311261P.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Yang Y, Wang Z, Weng G, Ma Y.

XX WPI; 2003-876918/81.

DR N-PSDB; ADF59603.

XX New polynucleotides, useful as hybridization probes, oligomers or  
PT primers, for chromosome or gene mapping, for the recombinant production  
PT of proteins, and for generating antisense DNA or RNA.

XX Claim 20; SEQ ID NO 2052; 571pp; English.

CC The present sequence represents a polypeptide (II) with biological  
CC activity, which is encoded by an isolated polynucleotide sequence (I)  
CC from the present invention. Also described: (1) a vector comprising (I);  
CC (2) an expression vector comprising (I); (3) a host cell genetically  
CC engineered to comprise (I) which is operatively associated with a  
CC regulatory sequence that modulates expression of (I) in the host cell;  
CC (4) a polypeptide (II) encoded by (I); (5) a composition comprising the  
CC polypeptide of (4) and a carrier; (6) an antibody directed against the  
CC polypeptide of (4); (7) detecting (I) or the polypeptide of (4) in a  
CC sample; (8) identifying a compound that binds to the polypeptide of (4);  
CC (9) producing the polypeptide of (4); and (10) a collection of  
CC polynucleotides comprising at least one of the polynucleotide sequences  
CC (I). The polynucleotides (I) can be used as hybridisation probes,  
CC oligomers or primers, for chromosome or gene mapping, for the recombinant  
CC production of proteins, and for generating antisense DNA or RNA.

XX SQ Sequence 350 AA;

Query Match 91.2%; Score 31; DB 7; Length 350;

Best Local Similarity 83.3%; Pred. No. 3.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6

Db 193 RRGFAY 198

Search completed: April 4, 2005, 15:47:20  
Job time : 13.9808 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 8.85623 seconds

(without alignments)  
224.651 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_99\_104

Perfect score: 34

Sequence: 1 RCFAY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
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19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	243	9	US-09-887-853-6
2	34	100.0	243	17	US-10-683-547-6
3	34	100.0	267	9	US-09-766-543-10
4	34	100.0	276	9	US-09-766-543-12
5	31	91.2	99	15	US-10-424-599-183438
6	31	91.2	122	15	US-10-424-599-170913
7	31	91.2	541	16	US-10-437-963-106568
8	31	91.2	1015	14	US-10-156-761-9633
9	31	91.2	1531	15	US-10-282-122A-49308
10	30	88.2	92	15	US-10-424-599-204252
11	30	88.2	738	15	US-10-369-493-2442
12	30	88.2	858	9	US-09-815-242-10894
13	30	88.2	858	15	US-10-282-122A-57157

14	29	85.3	60	15	US-10-424-599-220145	Sequence 220145,
15	29	85.3	65	15	US-10-424-599-208245	Sequence 208245,
16	29	85.3	88	15	US-10-424-599-161896	Sequence 161896,
17	29	85.3	148	16	US-10-437-963-132767	Sequence 132767,
18	29	85.3	153	15	US-10-424-599-159963	Sequence 159963,
19	29	85.3	191	16	US-10-767-701-33660	Sequence 33660, A
20	29	85.3	205	16	US-10-437-963-183461	Sequence 183461,
21	29	85.3	231	15	US-10-425-114-63712	Sequence 63712, A
22	29	85.3	250	15	US-10-282-122A-50355	Sequence 50355, A
23	29	85.3	252	15	US-10-425-114-60100	Sequence 60100, A
24	29	85.3	261	15	US-10-425-114-51324	Sequence 51324, A
25	29	85.3	288	9	US-09-815-242-11689	Sequence 11689, A
26	29	85.3	296	14	US-10-002-631C-40	Sequence 40, App1
27	29	85.3	340	15	US-10-282-122A-53110	Sequence 53110, A
28	29	85.3	342	15	US-10-282-122A-68785	Sequence 68785, A
29	29	85.3	343	15	US-10-425-114-44952	Sequence 44952, A
30	29	85.3	433	16	US-10-437-963-125372	Sequence 125372,
31	29	85.3	462	15	US-10-282-122A-51118	Sequence 51118, A
32	29	85.3	495	15	US-10-369-493-12829	Sequence 12829, A
33	29	85.3	503	16	US-10-767-701-44045	Sequence 44045, A
34	29	85.3	541	9	US-09-731-872-278	Sequence 278, App
35	29	85.3	541	9	US-09-731-872-282	Sequence 282, App
36	29	85.3	541	9	US-09-731-872-300	Sequence 300, App
37	29	85.3	541	10	US-09-876-997-278	Sequence 278, App
38	29	85.3	541	10	US-09-876-997-282	Sequence 282, App
39	29	85.3	541	10	US-09-876-997-300	Sequence 300, App
40	29	85.3	541	15	US-10-291-285-238	Sequence 238, App
41	29	85.3	549	15	US-10-369-493-3466	Sequence 3466, App
42	29	85.3	558	15	US-10-275-026A-112	Sequence 112, App
43	29	85.3	564	14	US-10-156-761-6951	Sequence 6951, App
44	29	85.3	603	16	US-10-437-963-125750	Sequence 125750,
45	29	85.3	637	15	US-10-369-493-21603	Sequence 21603, A

#### ALIGNMENTS

RESULT 1  
US-09-887-853-6  
Sequence 6, Application US/09887853  
Patent No. US20020168375A1  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
Oppermann, Hermann  
Houston, L. L.  
Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Teasca, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/887,853  
FILING DATE: 21-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/133,804  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-887-853-6

Query Match 100.0%; Score 34; DB 9; Length 243;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6  
DB 99 RFGPAY 104

RESULT 2  
US-10-683-547-6  
Sequence 6, Application US/10683547  
Publication No. US2005008638A1  
GENERAL INFORMATION:  
APPLICANT: Houston, J.  
APPLICANT: Houston, L.L.  
APPLICANT: Ring, D.  
APPLICANT: Oppermann, H.  
TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING  
FILE REFERENCE: C1BT-P01-130  
CURRENT APPLICATION NUMBER: US/10/683,547  
CURRENT FILING DATE: 2003-10-10  
PRIOR APPLICATION NUMBER: US/09/558,741  
PRIOR FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: 07/831,967  
PRIOR FILING DATE: 1992-02-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 520C9 sfv  
US-10-683-547-6

Query Match 100.0%; Score 34; DB 17; Length 243;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6  
DB 99 RFGPAY 104

RESULT 3  
US-09-766-543-10  
Sequence 10, Application US/09766543  
Patent No. US20020041865A1  
GENERAL INFORMATION:  
APPLICANT: Austin, Richard  
APPLICANT: Kwok, Cheuk S.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: METHODS FOR TREATING TUMORS  
FILE REFERENCE: PP01679.002  
CURRENT APPLICATION NUMBER: US/09/766,543  
CURRENT FILING DATE: 2000-01-19  
PRIOR APPLICATION NUMBER: 60/177,258  
PRIOR FILING DATE: 2000-01-20  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10

LENGTH: 267  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: 520C9  
OTHER INFORMATION: humanized single-chain antibody used in the  
OTHER INFORMATION: IL-2-antibody fusions  
US-09-766-543-10

Query Match 100.0%; Score 34; DB 9; Length 267;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6  
DB 121 RFGPAY 126

RESULT 4  
US-09-766-543-12  
Sequence 12, Application US/09766543  
Patent No. US20020041865A1  
GENERAL INFORMATION:  
APPLICANT: Austin, Richard  
APPLICANT: Kwok, Cheuk S.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: METHODS FOR TREATING TUMORS  
FILE REFERENCE: PP01679.002  
CURRENT APPLICATION NUMBER: US/09/766,543  
CURRENT FILING DATE: 2000-01-19  
PRIOR APPLICATION NUMBER: 60/177,258  
PRIOR FILING DATE: 2000-01-20  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 276  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: H520C9sfv plus  
OTHER INFORMATION: linker  
US-09-766-543-12

Query Match 100.0%; Score 34; DB 9; Length 276;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6  
DB 121 RFGPAY 126

RESULT 5  
US-10-424-599-183438  
Sequence 183438, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovacic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 183438  
LENGTH: 99  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_13658C.1.pcp

US-10-424-599-183438

Query Match 91.2%; Score 31; DB 15; Length 99;  
Best Local Similarity 83.3%; Pred. No. 79;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6  
:|||||  
Db 26 KRGPAY 31

RESULT 6

US-10-424-599-170913  
; Sequence 170913, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 170913  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_125349C.1.Dep  
US-10-424-599-170913

Query Match 91.2%; Score 31; DB 15; Length 122;  
Best Local Similarity 83.3%; Pred. No. 96;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6  
:|||||  
Db 82 KRGPAY 87

RESULT 7

US-10-437-963-106568  
; Sequence 106568, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 106568  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(541)  
; OTHER INFORMATION: unsure at all Xaa locations  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_109C.1.dep  
US-10-437-963-106568

Query Match 91.2%; Score 31; DB 16; Length 541;  
Best Local Similarity 83.3%; Pred. No. 41e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6  
|||||:  
Db 323 RGFSSY 328

RESULT 8

US-10-156-761-9633  
; Sequence 9633, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 9633  
; LENGTH: 1015  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-9633

Query Match 91.2%; Score 31; DB 14; Length 1015;  
Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6  
|||||:  
Db 541 RTGFAY 546

RESULT 9

US-10-282-122A-49308  
; Sequence 49308, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26

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; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49308
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (611)..(611)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (612)..(612)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (613)..(613)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (614)..(614)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (615)..(615)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (616)..(616)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (617)..(617)
; OTHER INFORMATION: X=any amino acid
US-10-282-122A-49308

Query Match          91.2%; Score 31; DB 15; Length 1531;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RFGFAY 6
Db      888 RYGFAY 893

RESULT 10
US-10-424-599-204252
; Sequence 204252, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
```

```

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 204252
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_26467C.1.pep
US-10-424-599-204252

Query Match          88.2%; Score 30; DB 15; Length 92;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RFGFAY 6
Db      73 RYGFAY 78

RESULT 11
US-10-369-493-2442
; Sequence 2442, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2442
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(738)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2442

Query Match          88.2%; Score 30; DB 15; Length 738;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RFGFAY 6
Db      148 RYGFAY 153

RESULT 12
US-09-815-242-10894
; Sequence 10894, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zysek, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
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/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10894
/ LENGTH: 858
/ TYPE: PRT
/ ORGANISM: Enterococcus faecalis
/ US-09-815-242-10894

Query Match
Best Local Similarity 88.2%; Score 30; DB 9; Length 858;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6
Db 139 QRGFAY 144

RESULT 13
/ US-10-282-122A-57157
/ Sequence 57157, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangou
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl
/ APPLICANT: Zykkind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Foreyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
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/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 57157
/ LENGTH: 858
/ TYPE: PRT
/ ORGANISM: Enterococcus faecalis
/ US-10-282-122A-57157

Query Match
Best Local Similarity 88.2%; Score 30; DB 15; Length 858;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6
Db 139 QRGFAY 144

RESULT 14
/ US-10-424-599-220145
/ Sequence 220145, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J
/ APPLICANT: Kovalic, David K
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 220145
/ LENGTH: 60
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_4081C.1.pep
/ US-10-424-599-220145

Query Match
Best Local Similarity 85.3%; Score 29; DB 15; Length 60;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGFAY 6
Db 31 RRGFAY 36

RESULT 15
/ US-10-424-599-208245
/ Sequence 208245, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J
/ APPLICANT: Kovalic, David K
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 208245
/ LENGTH: 65
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_30070C.1.pep
/ US-10-424-599-208245
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Query Match 85.3%; Score 29; DB 15; Length 65;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FGFAY 6  
 |||||  
 Db 41 FGFAY 45

Search completed: April 4, 2005, 16:42:46  
 Job time : 9.85623 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 15:32:36 ; Search time 2.16613 seconds  
(without alignments)  
266.512 Million cell updates/sec

Title: US-09-887-853-6\_COPY\_99\_104

Perfect score: 34

Sequence: 1 RRGFAY 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	91.2	48	2	AC0228
2	31	91.2	208	1	S26196
3	31	91.2	1008	2	G82732
4	30	88.2	177	2	T42289
5	30	88.2	213	2	S73011
6	30	88.2	336	2	G87202
7	30	88.2	356	2	C70025
8	30	88.2	468	2	D83625
9	30	88.2	776	2	S45495
10	29	85.3	98	2	F90362
11	29	85.3	98	2	B99358
12	29	85.3	137	2	S42467
13	29	85.3	164	2	G81321
14	29	85.3	174	2	G64413
15	29	85.3	213	2	E90356
16	29	85.3	273	2	D96920
17	29	85.3	283	2	E90524
18	29	85.3	299	2	T47003
19	29	85.3	299	2	AF0238
20	29	85.3	330	2	F69471
21	29	85.3	336	2	S74424
22	29	85.3	387	2	D84700
23	29	85.3	387	2	D84424
24	29	85.3	404	2	S27339
25	29	85.3	558	2	E81037
26	29	85.3	558	2	E81981
27	29	85.3	599	2	S15789
28	29	85.3	637	2	D75123
29	29	85.3	669	2	T28028

30	29	85.3	676	2	F69394	H+-transporting AT
31	29	85.3	696	2	G88851	protein ZK829.10 (
32	29	85.3	760	2	T01441	hypothetical prote
33	29	85.3	778	2	H96649	protein F2401.4 [1
34	29	85.3	843	2	T34618	NADH2 dehydrogenas
35	29	85.3	998	1	QOBBB1	B1 protein - black
36	29	85.3	998	2	S41397	protein A - flock
37	28	82.4	126	2	G83571	conserved hypothet
38	28	82.4	172	2	A27220	trypsin inhibitor
39	28	82.4	172	2	A24082	trypsin inhibitor
40	28	82.4	172	2	JH0780	trypsin inhibitor
41	28	82.4	205	2	E70199	competence protein
42	28	82.4	237	2	T16471	hypothetical prote
43	28	82.4	295	2	E72462	probable lipolic ac
44	28	82.4	339	2	A97699	sqdk protein [U453
45	28	82.4	365	2	AF2893	glycosyltransferase

#### ALIGNMENTS

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RESULT 1
AC0228
hypothetical protein YP01870 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #ext_change 09-Jul-2004
C/Accession: AC0228
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;
demo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
M., J.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, E
Nature 413, 523-527, 2001
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11585360
A:Accession: AC0228
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-48 <NR>
A:Cross-references: UNIPROT:Q8ZF48; GB:AL590842; PIDN:CA090687.1; PID:G15979892; GSPDB:G
C:Accession: AC0228
A:Gene: YP01870

Query Match
Best Local Similarity 91.2% Score 31; DB 2; Length 48;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6
Db 30 RRGFAY 35

RESULT 2
S26196
imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) - fungus (Trichoderma harzianum)
C:Species: Trichoderma harzianum
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 09-Jul-2004
C/Accession: S26196; S19787
R:Goldman, G.H.; Demolder, J.; Dewaele, S.; Herrera-Batrelia, A.; Geremia, R.A.; van Mont
Mol. Gen. Genet. 234, 481-488, 1992
A>Title: Molecular cloning of the imidazoleglycerol-phosphate dehydratase gene of Trichode
A:Reference number: S26196; MUID:93024323; PMID:1406594
A:Accession: S26196
A:Molecule type: mRNA
A:Residues: 1-208 <GOL>
A:Cross-references: UNIPROT:P34041; EMBL:Z11528; NID:G5176; PIDN:CAA77617.1; PID:G5177
C:Gene: igh
C:Superfamily: imidazoleglycerol-phosphate dehydratase; imidazoleglycerol-phosphate dehy
C:Keywords: carbon-oxygen lyase; histidine biosynthesis; hydro-lyase
F:58-208/Domain: imidazoleglycerol-phosphate dehydratase homology <IDP>

Query Match
Best Local Similarity 91.2% Score 31; DB 1; Length 208;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RFGFAY 6  
Db 120 RFGFAY 125

## RESULT 3

hypothetical protein XFI036 [imported] - Xylella fastidiosa (strain 9a5c)  
C/Species: Xylella fastidiosa  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C/Accession: G82732  
R/Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A/Reference number: A82515; MUID:20365717; PMID:10910347  
A/Note: for a complete list of authors see reference number A59328 below  
A/Accession: G82732  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1008 <SIM>  
A/Cross-references: UNIPROT:Q9PEJ2; GB:AE003940; GB:AE003849; MID:G9105966; PIDN:AAF8384  
A/Experimental source: strain 9a5c  
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvares, R.; Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carreir, H as-Neto, E.; Docena, C.; El-Dorri, H.; Facinani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitzima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Rodrigues, V.; Rosa, A.J. de M.; de Silva, F.R.; de Sa, R.G.; Senteilly, R.V.; Sawaak M.; Tshakko, M.H.; Vallada, H.; Van Sluys, W.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A/Reference number: A59328  
A/Contents: annotation  
C/Genetics:  
A/Gene: XFI036

Query Match 91.2%; Score 31; DB 2; Length 1008;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGFAY 6  
Db 636 RFGFAY 641

## RESULT 4

T42289  
hypothetical protein - phage SPPI  
C/Species: phage SPPI  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C/Accession: T42289  
R/Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.  
Gene 204, 201-212, 1997  
A/Title: The complete nucleotide sequence and functional organization of Bacillus subtilis A/Reference number: Z22137; MUID:98094274; PMID:9334185  
A/Accession: T42289  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-177 <ALDO>  
A/Cross-references: UNIPROT:O48449; EMBL:X97918; PIDN:CAA6550.1

Query Match 88.2%; Score 30; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 36;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGFAY 6  
Db 107 RFGFAY 112

## RESULT 5

S73011  
hypothetical protein L518\_C3\_195 - Mycobacterium leprae  
C/Species: Mycobacterium leprae  
C/Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C/Accession: S73011  
R/Smith, D.R.; Robison, K.  
submitted to the EMBL Data Library, November 1993  
A/Description: Mycobacterium leprae cosmid L518.  
A/Reference number: S72591  
A/Accession: S73011  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-213 <SM1>  
A/Cross-references: UNIPROT:Q49930; EMBL:U00023; MID:g467194; PIDN:AAA17354.1; PID:g4671 A/Start codon: GTG  
C/Superfamily: Mycobacterium leprae hypothetical protein L518\_C3\_195

Query Match 88.2%; Score 30; DB 2; Length 213;  
Best Local Similarity 83.3%; Pred. No. 43;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGFAY 6  
Db 42 RFGFAY 47

## RESULT 6

G87202  
probable membrane protein [imported] - Mycobacterium leprae  
C/Species: Mycobacterium leprae  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C/Accession: G87202  
R/Cole, S.T.; Biggmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.  
Nature 409, 1007-1011, 2001  
A/Authors: Ruter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq A/Title: Massive gene decay in the leprosy bacillus.  
A/Reference number: A86909; MUID:21128732; PMID:11234002  
A/Accession: G87202  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-336 <STO>  
A/Cross-references: UNIPROT:O69510; GB:AL450380; MID:g13093956; PIDN:CAC31863.1; GSPDB:G A/Genetics:  
A/Gene: ML2347

Query Match 88.2%; Score 30; DB 2; Length 336;  
Best Local Similarity 83.3%; Pred. No. 68;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGFAY 6  
Db 42 RFGFAY 47

## RESULT 7

C70025  
multidrug-efflux transporter homolog yuxJ - Bacillus subtilis  
N/Alternate names: mayB homolog, pbpD 5'-region  
C/Species: Bacillus subtilis  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: C70025; C55220  
R/Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berier C/Authors: Broer, S.; Brouillet, S.; Brunsch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Ehrlich, S.D.; Emmerson, P.T.; Ertian, K.D.; Errington, J.; Fabrec, C.; Ferrati, E. Nature 390, 249-256, 1997  
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y. M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Riva, C.; Rocha, A.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot  
Akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K  
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: C70025  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-356 <KUN>  
A:Cross-references: UNIPROT:P40760; GB:Z99120; GB:AL009126; NID:g2635613; PIDN:CAB15137.  
A:Experimental source: strain 168  
R:Popham, D.L.; Setlow, P.  
J. Bacteriol. 176, 7197-7205, 1994  
A:Title: Cloning, nucleotide sequence, mutagenesis, and mapping of the *Bacillus subtilis*  
A:Reference number: A55220; MUID:95050302; PMID:7961491  
A:Accession: C55220  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 101-356 <ROP>  
A:Cross-references: GB:U11882; NID:9520534; PIDN:AAA64942.1; PID:9520535  
A:Genetics:  
A:Gene: yuxJ  
C:Superfamily: Escherichia coli probable integral membrane protein  
Query Match 88.2%; Score 30; DB 2; Length 356;  
Best Local Similarity 83.3%; Pred. No. 72;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 RRGFAY 6  
DB 114 RRGFTY 119  
RESULT 8  
D83625  
Probable transporter PA0166 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C:Species: *Pseudomonas aeruginosa*  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: D83625  
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bz  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lim,  
.i. Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: D83625  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-468 <STO>  
A:Cross-references: UNIPROT:Q916W6; GB:AE004454; GB:AE004091; NID:g9945990; PIDN:AA0355  
A:Experimental source: strain PA01  
A:Genetics:  
A:Gene: PA0166  
Query Match 88.2%; Score 30; DB 2; Length 468;  
Best Local Similarity 83.3%; Pred. No. 95;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRGFAY 6  
DB 245 RRGFAF 250  
RESULT 9  
S845495  
Isop4 protein - fission yeast (*Schizosaccharomyces pombe*)  
C:Species: *Schizosaccharomyces pombe*  
C>Date: 10-Dec-1994 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: S845495, S83741

R:Sato, S.; Suzuki, H.; Widyastuti, U.; Hotta, Y.; Tabata, S.  
Curr. Genet. 26, 31-37, 1994  
A:Title: Identification and characterization of genes induced during sexual differentiation  
A:Reference number: S845492; MUID:95042833; PMID:7954893  
A:Accession: S845495  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-776 <SAT>  
A:Cross-references: UNIPROT:P40900; EMBL:D14061; NID:g218542; PIDN:BAA03147.1; PID:g21854  
C:Genetics:  
A:Gene: isp4  
C:Superfamily: *Saccharomyces cerevisiae* probable membrane protein YJL212c  
Query Match 88.2%; Score 30; DB 2; Length 776;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 RRGFAY 6  
DB 195 RRGFGY 200  
RESULT 10  
F90362  
Hypothetical protein SS09368 [imported] - *Sulfolobus solfataricus* transposon ISCT1913  
C:Species: *Sulfolobus solfataricus*  
C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C:Accession: F90362  
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Y  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A:Description: *Sulfolobus solfataricus* complete genome.  
A:Reference number: A99139  
A:Accession: F90362  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-98 <KUR>  
A:Cross-references: UNIPROT:Q97WZ4; GB:AE006641; NID:g13815241; PIDN:AAK42157.1; GSPDB:GT  
A:Genetics:  
A:Gene: SS09368  
Query Match 85.3%; Score 29; DB 2; Length 98;  
Best Local Similarity 83.3%; Pred. No. 32;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 RRGFAY 6  
DB 20 RRGFEY 25  
RESULT 11  
B99358  
Hypothetical protein SS09270 [imported] - *Sulfolobus solfataricus* transposon ISCT1913  
C:Species: *Sulfolobus solfataricus*  
C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C:Accession: B99358  
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Y  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A:Description: *Sulfolobus solfataricus* complete genome.  
A:Reference number: A99139  
A:Accession: B99358  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-98 <KUR>  
A:Cross-references: UNIPROT:Q97XZ7; GB:AE006641; NID:g13815199; PIDN:AAK42121.1; GSPDB:GT  
A:Genetics:  
A:Gene: SS09270  
Query Match 85.3%; Score 29; DB 2; Length 98;  
Best Local Similarity 83.3%; Pred. No. 32;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFGPAY 6  
|||||

Db 20 RGFEX 25

## RESULT 12

S42467

Ig heavy chain V region precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S42467

R:Shiyanov, P.A.; Beshpalov, I.A.; Tenletskaya, H.N.; Deyev, S.M.

submitted to the EMBL Data Library, March 1994

A:Reference number: S42466

A:Accession: S42467

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-137 &lt;SH1&gt;

A:Cross-references: EMBL:X78107; NID:g460798; PIDN:CAA5497.1; PID:g460799

C:Superfamily: immunoglobulin V region; immunoglobulin

C:Keywords: heterotetramer; immunoglobulin

F:34-119/Domain: immunoglobulin homology &lt;1MM&gt;

Query Match 85.3%; Score 29; DB 2; Length 137;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFGPAY 6  
|||||

Db 122 RFGPAY 126

## RESULT 13

G81321

probable integral membrane protein Cj1165c [imported] - Campylobacter jejuni (strain NCT

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C:Accession: G81321

R:Parhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quill, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: A81250; WUID:20150912; PMID:10688204

A:Accession: G81321

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-164 &lt;PAR&gt;

A:Cross-references: UNIPROT:Q9PND0; GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB7341

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: Cj1165c

C:Superfamily: primosomal operon 14K protein

Query Match 85.3%; Score 29; DB 2; Length 164;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFGPAY 6  
|||||

Db 17 RFGPAY 21

## RESULT 14

F64413

hypothetical protein M70910 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004

C:Accession: F64413

R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,

i Reich, C.I.; Overbeek, R.; Kirsch, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodex, A.;

reson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.

A:Reference number: A64300; WUID:96337999; PMID:8688087

A:Accession: F64413

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-174 &lt;BU1&gt;

A:Cross-references: UNIPROT:Q58320; GB:U67534; GB:L77117; NID:g1591579; PIDN:AAB98912.1;

C:Genetics:

A:Map position: REV841956-841432

Query Match 85.3%; Score 29; DB 2; Length 174;

Best Local Similarity 83.3%; Pred. No. 57;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFGPAY 6  
|||||

Db 147 RGFEX 152

## RESULT 15

E90356

hypothetical protein SSO1915 [imported] - Sulfolobus solfataricus transposon ISC1913

C:Species: Sulfolobus solfataricus

C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004

C:Accession: E90356

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweez, M.J.; Chan-Y

Jong, I.; Jeffries, A.C.; Kozera, C.D.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.

arrett, R.A.; Ragan, M.A.; Jensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: E90356

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-213 &lt;KUR&gt;

A:Cross-references: UNIPROT:Q97X40; GB:AE006641; NID:g13815184; PIDN:AAK42108.1; GSPDB:GT

C:Genetics:

A:Gene: SSO1915

Query Match 85.3%; Score 29; DB 2; Length 213;

Best Local Similarity 83.3%; Pred. No. 70;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFGPAY 6  
|||||

Db 135 RGFEX 140

Search completed: April 4, 2005, 15:58:05

Job time : 3.16613 secs



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RA Niranjanaki A., Banks G.K., Frohlich D., Veneti D.R., Braig H.R.,  
RA Miller T.A., Bedford I.D., arkham P.G., Savakis C., Bourtzis K.,  
RT "Wolbachia infections of the whitefly Bemisia tabaci."  
RL Curr. Microbiol. 47:93-101(2003).  
DR EMBL; AJ291377; CAC44877.1; "-"  
DR InterPro; IPR002566; Surface_Ag_msp4.  
DR Pfam; PF01617; Surface_Ag_2; 2.  
FT NON_TER 1 185  
SQ SEQUENCE 185 AA; 19843 MW; F2209E49DF904F58 CRC64;  
  
Query Match 100.0%; Score 34; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RFGPAY 6  
Db 128 RFGPAY 133
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RESULT 3  
Q93IJ2 PRELIMINARY; PRT; 185 AA.  
ID Q93IJ2  
AC Q93IJ2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Outer surface protein (Fragment).  
GN Name=msp;  
OS Wolbachia sp. wBtab4.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Wolbachiae; Wolbachia.  
OX NCBI_TaxID=133460;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=wBtab4;  
RX MEDLINE=22867875; PubMed=14506854;  
RA Niranjanaki A., Banks G.K., Frohlich D., Veneti D.R., Braig H.R.,  
RA Miller T.A., Bedford I.D., arkham P.G., Savakis C., Bourtzis K.,  
RT "Wolbachia infections of the whitefly Bemisia tabaci."  
RL Curr. Microbiol. 47:93-101(2003).  
DR EMBL; AJ291375; CAC44875.1; "-"  
DR InterPro; IPR002566; Surface_Ag_msp4.  
DR Pfam; PF01617; Surface_Ag_2; 2.  
FT NON_TER 1 185  
SQ SEQUENCE 185 AA; 19809 MW; F2209E49D3634F58 CRC64;  
  
Query Match 100.0%; Score 34; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RFGPAY 6  
Db 128 RFGPAY 133
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RX MEDLINE=22867875; PubMed=14506854;  
RA Niranjanaki A., Banks G.K., Frohlich D., Veneti D.R., Braig H.R.,  
RA Miller T.A., Bedford I.D., arkham P.G., Savakis C., Bourtzis K.,  
RT "Wolbachia infections of the whitefly Bemisia tabaci."  
RL Curr. Microbiol. 47:93-101(2003).  
DR EMBL; AJ291374; CAC44874.1; "-"  
DR InterPro; IPR002566; Surface_Ag_msp4.  
DR Pfam; PF01617; Surface_Ag_2; 2.  
FT NON_TER 1 185  
SQ SEQUENCE 185 AA; 19809 MW; F2209E49D3634F58 CRC64;  
  
Query Match 100.0%; Score 34; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RFGPAY 6  
Db 128 RFGPAY 133
```

```
RESULT 5  
Q9R8D2 PRELIMINARY; PRT; 185 AA.  
ID Q9R8D2  
AC Q9R8D2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Outer surface protein (Fragment).  
GN Name=msp;  
OS Wolbachia sp. wNub.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Wolbachiae; Wolbachia.  
OX NCBI_TaxID=77832;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=wNub;  
RX MEDLINE=99398205; PubMed=10469257;  
RA van Meer M.M.M., Witteveldt U., Stoutamer R.,  
RT "Phylogeny of the arthropod endosymbiont Wolbachia based on the msp  
RT gene."  
RL Insect Mol. Biol. 8:399-408(1999).  
DR EMBL; AF071928; AAC77406.1; "-"  
DR InterPro; IPR002566; Surface_Ag_msp4.  
DR Pfam; PF01617; Surface_Ag_2; 2.  
FT NON_TER 1 185  
SQ SEQUENCE 185 AA; 20030 MW; 48424234CCE60431 CRC64;  
  
Query Match 100.0%; Score 34; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RFGPAY 6  
Db 128 RFGPAY 133
```

```
RESULT 6  
Q9R8D3 PRELIMINARY; PRT; 185 AA.  
ID Q9R8D3  
AC Q9R8D3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Outer surface protein (Fragment).  
GN Name=msp;  
OS Wolbachia sp. wDeiSW.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Wolbachiae; Wolbachia.  
OX NCBI_TaxID=77831;  
RN [1]  
RP SEQUENCE FROM N.A.
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RC STRAIN=WD61SM;  
RA MEDLINE=99398205; PubMed=10469257;  
RX van Meer M.M.M., Witteveldt J., Stouthamer R.;  
RT "Phylogeny of the arthropod endosymbiont Wolbachia based on the wsp  
gene."  
RL Insect Mol. Biol. 8:399-408(1999).  
DR EMBL; AF071925; AAC77405.1; -;  
DR InterPro; IPR002566; Surface\_Ag\_msp4.  
DR Pfam; PF01617; Surface\_Ag\_2; 2.  
FT NON\_TER 1  
FT NON\_TER 185  
SQ SEQUENCE 185 AA; 20045 MW; 52F2439260ED0E91 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6  
Db 128 RFGPAY 133

## RESULT 7

Q9ZH44 PRELIMINARY; PRT; 185 AA.  
AC Q9ZH44;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Outer surface protein (Fragment).  
GN Name=WSP;  
OS Wolbachia sp. wKAYLC.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Wolbachiae; Wolbachia.  
OX NCBI\_TaxID=77833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WKAYLC.  
RC MEDLINE=99398205; PubMed=10469257;  
RX van Meer M.M.M., Witteveldt J., Stouthamer R.;  
RT "Phylogeny of the arthropod endosymbiont Wolbachia based on the wsp  
gene."  
RL Insect Mol. Biol. 8:399-408(1999).  
DR EMBL; AF071927; AAC77407.1; -;  
DR InterPro; IPR002566; Surface\_Ag\_msp4.  
DR Pfam; PF01617; Surface\_Ag\_2; 2.  
FT NON\_TER 1  
FT NON\_TER 185  
SQ SEQUENCE 185 AA; 19990 MW; 1F1D66A2B72FA662 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6  
Db 128 RFGPAY 133

## RESULT 8

Q9ZH45 PRELIMINARY; PRT; 185 AA.  
AC Q9ZH45;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Outer surface protein (Fragment).  
GN Name=WSP;  
OS Wolbachia sp. wKAYB.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Wolbachiae; Wolbachia.  
OX NCBI\_TaxID=77830;  
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=WKAYB;  
RX MEDLINE=99398205; PubMed=10469257;  
RA van Meer M.M.M., Witteveldt J., Stouthamer R.;  
RT "Phylogeny of the arthropod endosymbiont Wolbachia based on the wsp  
gene."  
RL Insect Mol. Biol. 8:399-408(1999).  
DR EMBL; AF071924; AAC77404.1; -;  
DR InterPro; IPR002566; Surface\_Ag\_msp4.  
DR Pfam; PF01617; Surface\_Ag\_2; 2.  
FT NON\_TER 1  
FT NON\_TER 185  
SQ SEQUENCE 185 AA; 20044 MW; 52F2439FDEDD0E91 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6  
Db 128 RFGPAY 133

## RESULT 9

Q9ZH46 PRELIMINARY; PRT; 185 AA.  
AC Q9ZH46;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Outer surface protein (Fragment).  
GN Name=WSP;  
OS Wolbachia sp. wSib.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Wolbachiae; Wolbachia.  
OX NCBI\_TaxID=77829;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WSib;  
RC MEDLINE=99398205; PubMed=10469257;  
RX van Meer M.M.M., Witteveldt J., Stouthamer R.;  
RT "Phylogeny of the arthropod endosymbiont Wolbachia based on the wsp  
gene."  
RL Insect Mol. Biol. 8:399-408(1999).  
DR EMBL; AF071923; AAC77403.1; -;  
DR InterPro; IPR002566; Surface\_Ag\_msp4.  
DR Pfam; PF01617; Surface\_Ag\_2; 2.  
FT NON\_TER 1  
FT NON\_TER 185  
SQ SEQUENCE 185 AA; 19997 MW; 93E9C36F2F8F6F19 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6  
Db 128 RFGPAY 133

## RESULT 10

Q9LSY4 PRELIMINARY; PRT; 186 AA.  
AC Q9LSY4;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Outer surface protein (Fragment).  
GN Name=WSP;  
OS Bacteria; endosymbiont of Trichogramma evanescens.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Wolbachiae; Wolbachia.  
OX NCBI\_TaxID=125597;

```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M36;
RX MEDLINE=20496957; PubMed=11040288;
RA Pintureau B., Chaudier S., Lassabliere F., Charles H., Grenier S.;
RT "Addition of wsp sequences to the Wolbachia phylogenetic tree and
RL stability of the classification.";
RL J. Mol. Evol. 51:374-377(2000).
DR EMBL; AF245167; AAF71321.1; -.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 2.
FT NON_TER
FT NON_TER
SQ SEQUENCE 186 AA; 20088 MW; 911EAFABDF6451DF CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 2; Length 186;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6
DB 129 RRGFAY 134

RESULT 11
Q9L5Y5 PRELIMINARY; PRT; 186 AA.
AC Q9L5Y5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE Outer surface protein (Fragment).
GN Name=wsp;
OS Wolbachia endosymbiont of Trichogramma oleae.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxID=125596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M32;
RX MEDLINE=20496957; PubMed=11040288;
RA Pintureau B., Chaudier S., Lassabliere F., Charles H., Grenier S.;
RT "Addition of wsp sequences to the Wolbachia phylogenetic tree and
RL stability of the classification.";
RL J. Mol. Evol. 51:374-377(2000).
DR EMBL; AF245166; AAF71320.1; -.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 2.
FT NON_TER
FT NON_TER
SQ SEQUENCE 186 AA; 20144 MW; 230A17BA67089A91 CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 2; Length 186;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6
DB 129 RRGFAY 134

RESULT 12
Q9L5Y7 PRELIMINARY; PRT; 186 AA.
AC Q9L5Y7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE Outer surface protein (Fragment).
GN Name=wsp;
OS Wolbachia endosymbiont of Trichogramma cordubensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
```

```
OX NCBI_TaxID=125594;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Grey;
RX MEDLINE=20496957; PubMed=11040288;
RA Pintureau B., Chaudier S., Lassabliere F., Charles H., Grenier S.;
RT "Addition of wsp sequences to the Wolbachia phylogenetic tree and
RL stability of the classification.";
RL J. Mol. Evol. 51:374-377(2000).
DR EMBL; AF245164; AAF71318.1; -.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 2.
FT NON_TER
FT NON_TER
SQ SEQUENCE 186 AA; 20088 MW; 911EAFABDF6451DF CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 2; Length 186;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6
DB 129 RRGFAY 134

RESULT 13
Q9L5Y8 PRELIMINARY; PRT; 186 AA.
AC Q9L5Y8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE Outer surface protein (Fragment).
GN Name=wsp;
OS Wolbachia endosymbiont of Trichogramma pretiosum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxID=125593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T191;
RX MEDLINE=20496957; PubMed=11040288;
RA Pintureau B., Chaudier S., Lassabliere F., Charles H., Grenier S.;
RT "Addition of wsp sequences to the Wolbachia phylogenetic tree and
RL stability of the classification.";
RL J. Mol. Evol. 51:374-377(2000).
DR EMBL; AF245163; AAF71317.1; -.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 2.
FT NON_TER
FT NON_TER
SQ SEQUENCE 186 AA; 20144 MW; 230A17BA67089A91 CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 2; Length 186;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6
DB 129 RRGFAY 134

RESULT 14
Q9L5Y9 PRELIMINARY; PRT; 186 AA.
AC Q9L5Y9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE Outer surface protein (Fragment).
GN Name=wsp;
OS Wolbachia endosymbiont of Trichogramma semblidis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
```

```
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxId=125592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=semv;
RX MEDLINE=20496957; PubMed=11040288;
RA Pintureau B., Chaudier S., Laesabliere F., Charles H., Grenier S.;
RT "Addition of wsp sequences to the Wolbachia phylogenetic tree and
RT stability of the classification.";
RL J. Mol. Evol. 51:374-377(2000).
DR EMBL; AF245162; AAF71316.1; -
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 2.
FT NON_TER 1 186
SQ SEQUENCE 186 AA; 20158 MW; 56013C0E2C07DFC8 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6
Db 129 RFGPAY 134

RESULT 15
O6GV15 PRELIMINARY; PRT; 190 AA.
ID O6GV15;
AC O6GV15;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Outer surface protein (Fragment).
GN Name=wsp;
OS Wolbachia endosymbiont of Trichogramma dendrolimi.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxId=164403;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang C.M., Cong B., Dai Q.H., Fu H.B.;
RL Submitted (MAY-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY634680; AAT48492.1; -
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 1.
FT NON_TER 1 190
SQ SEQUENCE 190 AA; 20614 MW; 1861F4336D01621 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6
Db 127 RFGPAY 132
```

Search completed: April 4, 2005, 15:56:21  
Job time : 12.1406 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: April 4, 2005, 15:19:49 ; Search time 485.224 Seconds  
(without alignments)  
193.690 Million cell updates/sec

Title: US-09-887-853-6

Perfect score: 1258

Sequence: 1 EIQLVQSGPELKKRGFTYKI.....YAIPFYTGSGTNLE..KRAD 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_16Dec04:\*  
1: geneeqqp19908:\*  
2: geneeqqp19908:\*  
3: geneeqqp20008:\*  
4: geneeqqp20018:\*  
5: geneeqqp20028:\*  
6: geneeqqp20038:\*  
7: geneeqqp20038:\*  
8: geneeqqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	100.0	243	2	AAW02280 520C9 ant
2	1258	100.0	243	2	AAW53170 520C9 ant
3	1258	100.0	243	2	AAW80424 520C9 bFv
4	1258	100.0	243	7	ABW00716 520C9 bFv
5	1258	100.0	246	2	AAW39569 Sequence
6	1206	95.9	534	2	AAW39571 Sequence
7	1055	83.9	409	4	AAU04845 Humanised
8	976	77.6	499	5	AAU72872 Humanised
9	950.5	75.6	267	4	AAU04944 Humanised
10	914	72.7	250	2	AAW02278 741F8 ant
11	914	72.7	250	2	AAW02278 741F8 ant
12	914	72.7	250	2	AAW22400 Single ch
13	914	72.7	250	2	AAW47012 Single ch
14	914	72.7	250	2	AAW53168 741F8 ant
15	914	72.7	250	2	AAW53168 741F8 ant
16	914	72.7	250	7	ABW00714 741F8 bFv
17	879	68.9	237	3	AAW39573 Sequence
18	857.5	68.2	237	3	AAW44595 bFv#125
19	857.5	68.2	243	3	AAW44596 bFv#125
20	857	68.1	259	7	ADG32322 Mouse bCF
21	857	68.1	329	7	ADG32322 Precursor
22	842	66.9	259	7	ADG32324 Mouse bCF
23	842	66.9	329	7	ADG32324 Precursor
24	841.5	66.9	240	8	ADN16154 Mouse C7
25	840.5	66.8	242	4	AAW20433 Anti-FIX/

26	830.5	66.0	461	2	AAW85508 Leader-sc
27	823.5	65.5	530	2	AAW95053 scFv(FRP5
28	823.5	65.5	615	2	AAW95056 GAL4-DT-8
29	823.5	65.5	617	2	AAW95057 GAL4-DT-8
30	823.5	65.5	651	2	AAW05136 scFv(FRP5
31	823.5	65.5	699	2	AAW05138 scFv(FRP5
32	823.5	65.5	711	2	AAW26980 Fv(FRP5) -
33	823.5	65.5	892	2	AAW05140 scFv2 (225
34	823.5	65.5	892	2	AAW05143 scFv2 (FRP
35	823.5	65.5	892	2	AAW05139 scFv2 (FRP
36	823.5	65.5	895	2	AAW05142 scFv2 (FRP
37	823.5	65.5	899	2	AAW05144 scFv2 (FRP
38	823.5	65.5	1020	2	AAW05141 scFv2 (FRP
39	820.5	65.2	637	2	AAW26982 (FRP5) -BT
40	818.5	65.1	240	2	AAW85494 bFv2-8P
41	818.5	65.1	240	2	AAW05134 Single ch
42	818	65.0	252	5	AAU72863 P4-14 bin
43	816	64.9	259	3	AAW09779 AntiVira1
44	815.5	64.8	251	7	ADG32321 Mouse bCF
45	815.5	64.8	320	7	ADG32358 Precursor

## ALIGNMENTS

RESULT 1					
AAW02280	AAW02280 standard; protein; 243 AA.				
ID					
XX					
AC	AAW02280;				
XX					
DT	25-MAR-2003 (revised)				
DT	29-OCT-1996 (first entry)				
XX					
DE	520C9 anti-c-erbB-2 two single chain Fv construct.				
XX					
KW	520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; bFv;				
KW	construct; polypeptide linker; C-terminal; amino acid sequence;				
KW	in vivo imaging; drug targeting experiment; homodimer; increased;				
KW	binding avidity; tissue retention time.				
XX					
OS	Homo sapiens.				
XX					
PH	Key				
FT	Peptide				
FT	Location/Qualifiers				
XX	118..133				
XX	/label= linker				
PN					
XX	US5534254-A.				
PD	09-JUL-1996.				
XX					
PF	07-OCT-1993; 93US-00133804.				
XX					
PR	06-FEB-1992; 92US-0081967.				
XX					
PA	(CHIR ) CHIRON CORP.				
PA	(CREA-) CREATIVE BIOMOLECULES INC.				
PI	Opfermann H, Ring DB, Huston JS, Houston LL;				
DR	WPI, 1996-333194/33.				
XX	N-PSDB; AAT36880.				
PT	Compan. contg. antigen-targeting antibody fragment constructs -				
PT	comprising dimer of single-chain Fv fragments.				
XX					
PS	Example 1; Col 33-36; 30pp; English.				
XX					
CC	Variable heavy (VH) and variable light (VL) genes were cloned from a				
CC	520C9 hybridoma cDNA library, using probes directed toward the antibody				
CC	construct and joining regions. A two single chain Fv (bFv) gene was				
CC	constructed by connecting the VH and VL genes with a Ser rich polypeptide				
CC	linker. The resulting 520C9 two bFv gene, which encodes the present				

CC sequence, was inserted into an expression vector, transformed into E.  
CC coli, and protein expression induced by the addn. of IPTG to the culture  
CC medium. A compsn. comprising a carrier and the 2 sfv protein prod. can be  
CC used for in vivo imaging, and drug targeting experiments. The 2 sfv  
CC protein prod. is a homodimer, in which both fragments target the same  
CC antigen, therefore giving greater binding avidity and longer tissue  
CC retention times, compared to individual sfv protein prod. fragments.  
CC (Updated on 25-MAR-2003 to correct PF field.)  
CC  
XX

Sequence 243 AA;

Query Match 100.0%; Score 1258; DB 2; Length 243;

Best Local Similarity 100.0%; Pred. No. 8.8e-88;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIQLVQSGPELKKPGETVTKISCKASGYTFPANYGMNMWKAQPGKGLKMWGINTYTGOSTY 60  
DB 1 EIQLVQSGPELKKPGETVTKISCKASGYTFPANYGMNMWKAQPGKGLKMWGINTYTGOSTY 60  
QY 61 ADPFKERFAPSLKETSATTAAHQLINNLNEDSATYFCARRFPFAVWGQGLVSVASISSS 120  
DB 61 ADPFKERFAPSLKETSATTAAHQLINNLNEDSATYFCARRFPFAVWGQGLVSVASISSS 120  
QY 121 SSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIKRL 180  
DB 121 SSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIKRL 180  
QY 181 IYATSSLDGVPKRPFGSGRSGSDYSLTISLSEDPFVYVYCLQYAIPTYPFGGNTLEIK 240  
DB 181 IYATSSLDGVPKRPFGSGRSGSDYSLTISLSEDPFVYVYCLQYAIPTYPFGGNTLEIK 240  
QY 241 RAD 243  
DB 241 RAD 243

RESULT 2

AAM53170

ID AAM53170 standard; protein; 243 AA.

XX AAM53170;

DT 16-JUL-1998 (first entry)

DE 520C9 anti-c-erbB-2 sfv' dimeric construct protein sequence.

XX Antigen imaging: single chain Fv; sfv; linker; dimeric; cancer; c-erbB-2;  
KM tumour; diagnosis; ss.

XX Synthetic.

OS Mus sp.

PN US5753204-A.

PD 19-MAY-1998.

PF 05-JUN-1995; 95US-00461838.

PR 06-FEB-1992; 92US-00831967.

PR 07-OCT-1993; 93US-00133804.

PA (CHIR ) CHIRON CORP.

PA (CREA-) CREATIVE BIOMOLECULES INC.

XX Oppermann H, Ring DB, Huston JS, Huston LL;

DR WPI; 1998-311318/27.

DR N-PSDB; AAV21798.

XX Imaging of antigens in vivo - using dimers of single-chain antibody Fv  
PT fragments.

PS Example 1; Col 33-36; 30pp; English.

XX This represents the protein sequence of a 520C9 sfv' (single chain Fv)  
CC construct. This was constructed by connecting the Vh and Vl genes with a  
CC DNA sequence encoding a Serine rich linker. 520C9 is a monoclonal  
CC antibody useful in targeting c-erbB-2 antigen. This dimeric construct can  
CC be used in the methods of invention of imaging a preselected antigen  
CC expressed in a mammal. The methods are used in magnetic resonance imaging  
CC of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic  
CC constructs have enhanced properties as in vivo targeting agents in  
CC comparison with intact monoclonal antibodies or their Fab fragments. The  
CC dimeric constructs permit the in vivo targeting of an epitope on an  
CC antigen with greater apparent avidity, including greater tumour  
CC specificity, tumour localisation and tumour retention properties than  
CC that of the Fab fragment having the same CDRs as the construct  
CC  
XX

Sequence 243 AA;

Query Match 100.0%; Score 1258; DB 2; Length 243;

Best Local Similarity 100.0%; Pred. No. 8.8e-88;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIQLVQSGPELKKPGETVTKISCKASGYTFPANYGMNMWKAQPGKGLKMWGINTYTGOSTY 60  
DB 1 EIQLVQSGPELKKPGETVTKISCKASGYTFPANYGMNMWKAQPGKGLKMWGINTYTGOSTY 60  
QY 61 ADPFKERFAPSLKETSATTAAHQLINNLNEDSATYFCARRFPFAVWGQGLVSVASISSS 120  
DB 61 ADPFKERFAPSLKETSATTAAHQLINNLNEDSATYFCARRFPFAVWGQGLVSVASISSS 120  
QY 121 SSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIKRL 180  
DB 121 SSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIKRL 180  
QY 181 IYATSSLDGVPKRPFGSGRSGSDYSLTISLSEDPFVYVYCLQYAIPTYPFGGNTLEIK 240  
DB 181 IYATSSLDGVPKRPFGSGRSGSDYSLTISLSEDPFVYVYCLQYAIPTYPFGGNTLEIK 240  
QY 241 RAD 243  
DB 241 RAD 243

RESULT 3

AAM80424

ID AAM80424 standard; protein; 243 AA.

XX AAM80424;

DT 28-JAN-1999 (first entry)

DE 520C9 sfv sequence.

XX 520C9 sfv; antigen; tumour cell; antibody 520C9; targeted delivery;

KM antigen-expressing cell.

XX Synthetic.

PN US5837846-A.

PD 17-NOV-1998.

PF 05-JUN-1995; 95US-00461838.

PR 06-FEB-1992; 92US-00831967.

PR 07-OCT-1993; 93US-00133804.

PA (CHIR ) CHIRON CORP.

PA (CREA-) CREATIVE BIOMOLECULES INC.

XX Oppermann H, Huston LL, Huston JS, Ring DB;

DR WPI; 1999-023541/02.

DR N-PSDB; AAV63399.

```
XX Nucleic acid encoding single-chain Fv fragment specific for antigens -
PT and having C-terminal tail for crosslinking to form dimer with improved
PT pharmacokinetic properties, used to deliver drugs and imaging agents,
PT especially to tumours.
XX
PS Example 1; Col 35-36; 29pp; English.
XX
CC The present sequence represents an antibody 520C9 eFv. Variable heavy and
CC light sequences of antibody 7520C9 are connected, together with a serine
CC linker, to produce the present single chain Fv gene. The present sequence
CC exemplifies the invention. Dimers of the single chain Fv are used for
CC targeted delivery of drugs or imaging agents (e.g. cytotoxic, prodrugs
CC or 39m-technetium) to antigen-expressing cells, particularly for
CC treatment or diagnosis of tumours (especially of ovary or breast)
CC
XX
SQ Sequence 243 AA;
XX
Query Match 100.0%; Score 1258; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 8.8e-88;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIQLVQSGELKKPGETVKISCKASGYTFANYGMNMMKQAPGKGLKMMGINTYTGQSTY 60
DB 1 EIQLVQSGELKKPGETVKISCKASGYTFANYGMNMMKQAPGKGLKMMGINTYTGQSTY 60
QY 61 ADDPKERFAFSLKTSATTATLQINLRNEDSATYFCARRFGFAVMQGTLVSVASISSS 120
DB 61 ADDPKERFAFSLKTSATTATLQINLRNEDSATYFCARRFGFAVMQGTLVSVASISSS 120
QY 121 SSSSSSSSSSGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 180
DB 121 SSSSSSSSSSGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 180
QY 181 IYATSSLDGVPKRFSGSRGSDYSLTISLSEDFVYVYCIQYAFPTFGGNTLEIK 240
DB 181 IYATSSLDGVPKRFSGSRGSDYSLTISLSEDFVYVYCIQYAFPTFGGNTLEIK 240
QY 241 RAD 243
DB 241 RAD 243
XX
RESULT 4
ABM00716
ID ABM00716 standard; protein; 243 AA.
XX
AC ABM00716;
XX
XX 15-JAN-2004 (first entry)
XX
DE 520C9 eFv protein.
XX
XX Cell proliferation; cytotoxic agent; drug targeting; single-chain Fv;
XX eFv.
XX
XX Unidentified.
XX
XX US2002168375-A1.
XX
XX 14-NOV-2002.
XX
XX 21-JUN-2001; 2001US-00887853.
XX
XX 06-FEB-1992; 92US-00831967.
XX PR 07-OCT-1993; 93US-00133804.
XX PR 05-JUN-1995; 95US-00462641.
XX PR 26-APR-2000; 2000US-00556741.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Huston JS, Houston LL, Ring DB, Oppermann H;
```

```
DR WPI: 2003-765156/72.
DR N-PSDB; AAD61485.
XX
XX Novel binding protein formulation for targeting epitope on antigen in
PT mammal, comprising dimeric biosynthetic construct having conformation
PT permitting binding of antigen by binding site of each polypeptide chain.
XX
PS Example 1; Page 19-20; 30pp; English.
XX
XX
CC The invention relates to a binding protein formulation for targeting an
CC epitope on an antigen expressed in mammal. The formulation comprises of
CC dimeric biosynthetic construct having conformation permitting binding of
CC antigen by binding site of each polypeptide chain. The invention is
CC useful for imaging a preselected antigen in a mammal expressing the
CC antigen. It is also useful for targeting drugs that inhibit cell
CC proliferation and cytotoxic agents that kill cells. The present sequence
CC is 520C9 eFv protein. This sequence is used in the exemplification of the
CC invention
CC
XX
SQ Sequence 243 AA;
XX
Query Match 100.0%; Score 1258; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 9.8e-88;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIQLVQSGELKKPGETVKISCKASGYTFANYGMNMMKQAPGKGLKMMGINTYTGQSTY 60
DB 1 EIQLVQSGELKKPGETVKISCKASGYTFANYGMNMMKQAPGKGLKMMGINTYTGQSTY 60
QY 61 ADDPKERFAFSLKTSATTATLQINLRNEDSATYFCARRFGFAVMQGTLVSVASISSS 120
DB 61 ADDPKERFAFSLKTSATTATLQINLRNEDSATYFCARRFGFAVMQGTLVSVASISSS 120
QY 121 SSSSSSSSSSGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 180
DB 121 SSSSSSSSSSGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 180
QY 181 IYATSSLDGVPKRFSGSRGSDYSLTISLSEDFVYVYCIQYAFPTFGGNTLEIK 240
DB 181 IYATSSLDGVPKRFSGSRGSDYSLTISLSEDFVYVYCIQYAFPTFGGNTLEIK 240
QY 241 RAD 243
DB 241 RAD 243
XX
RESULT 5
AAR39569
ID AAR39569 standard; protein; 246 AA.
XX
AC AAR39569;
XX
XX 25-MAR-2003 (revised)
XX DT 07-FEB-1994 (first entry)
XX
DE Sequence of 520C9 eFv protein.
XX
XX Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;
XX biosynthetic single polypeptide chain binding site; se.
XX
XX Synthetic.
XX
XX WO9316185-A2.
XX
XX 19-AUG-1993.
XX
XX 05-FEB-1993; 93WO-US001055.
XX
XX 06-FEB-1992; 92US-00831967.
XX
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX (CENTU ) CENTUS ONCOLOGY CORP.
```

PI Huston JS, Houston IL, Ring DB, Oppermann H;  
 XX WPI: 1993-272889/34.  
 DR N-PSDB; AA046084.  
 XX  
 PT New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for  
 XX imaging or treating breast or ovarian cancer etc.  
 PS  
 XX Claim 4; Page 60-61; 87pp; English.  
 CC C-erbB-2 refers to a protein antigen expressed on the surface of tumour  
 CC cells, such as breast and ovarian tumour cells, which is an approx.  
 CC 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about  
 CC 5.3 (see AA046083, AAR39568). A single chain Fv (scFv) is a covalently  
 CC linked VH-VL heterodimer which is expressed from a gene fusion including  
 CC VH- and VL- encoding genes connected by a peptide linker. Such  
 CC linker sequences are set forth in AA residues 116-135 in AAR39569, which  
 CC includes part of the 16 AA linker sequences in AAR39572. Using AA046084  
 CC for the 520C9 monoclonal antibody, a single chain polypeptide can be  
 CC produced having a binding affinity for a C-erbB-2 related antigen. 'X' in  
 CC AAR39569 refers to the location of a stop codon in AA046084. (Updated on  
 CC 25-MAR-2003 to correct PN field.)  
 CC  
 XX Sequence 246 AA;

Query Match 100.0%; Score 1258; DB 2; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 8,9e-88;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIQLVQSGPELKKRGETVTKISCKASGYTFPANYGNMWMKQAPGKGLKMWGINITYTGOSTY 60  
 DB 1 EIQLVQSGPELKKRGETVTKISCKASGYTFPANYGNMWMKQAPGKGLKMWGINITYTGOSTY 60  
 QY 61 ADPFKEFAFSLTETSAATHQINNLNEDSATYFCARRRFGFAWGGTIVSVASISSS 120  
 DB 61 ADPFKEFAFSLTETSAATHQINNLNEDSATYFCARRRFGFAWGGTIVSVASISSS 120  
 QY 121 SGSSSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIK 180  
 DB 121 SGSSSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIK 180  
 QY 181 IYVTSLSLDGVPKRFSGSRGSDYSLTISLESDPVVYVYCYOYAFPTTGGGNTLLEIK 240  
 DB 181 IYVTSLSLDGVPKRFSGSRGSDYSLTISLESDPVVYVYCYOYAFPTTGGGNTLLEIK 240  
 QY 241 RAD 243  
 DB 241 RAD 243

RESULT 6  
 AAR39571  
 ID AAR39571 standard; protein; 534 AA.  
 AC AAR39571;  
 XX  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-FEB-1994 (first entry)  
 XX  
 DE Sequence of G-FIT.  
 XX  
 KM Tumour antigen; C-erbB-2; G-FIT.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9316185-A2.  
 PD 19-AUG-1993.  
 XX  
 PF 05-FEB-1993; 93WO-US001055.  
 XX  
 PR 06-FEB-1992; 92US-00831967.  
 XX

PA (CREA-) CREATIVE BIOMOLECULES INC.  
 PA (CETU) CETUS ONCOLOGY CORP.  
 XX  
 XX Huston JS, Houston IL, Ring DB, Oppermann H;  
 XX WPI: 1993-272889/34.  
 DR N-PSDB; AA046086.  
 XX  
 PT New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for  
 XX imaging or treating breast or ovarian cancer etc.  
 PS  
 XX Example; Page 65-68; 87pp; English.

CC C-erbB-2 refers to a protein antigen expressed on the surface of tumour  
 CC cells, such as breast and ovarian tumour cells, which is an approx.  
 CC 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about  
 CC 5.3 (see AA046083, AAR39568). (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 CC  
 XX Sequence 534 AA;

Query Match 95.9%; Score 1206; DB 2; Length 534;  
 Best Local Similarity 95.1%; Pred. No. 2e-63;  
 Matches 233; Conservative 1; Mismatches 9; Indels 2; Gaps 1;

QY 1 EIQLVQSGPELKKRGETVTKISCKASGYTFPANYGNMWMKQAPGKGLKMWGINITYTGOSTY 60  
 DB 230 EIQLVQSGPELKKRGETVTKISCKASGYTFPANYGNMWMKQAPGKGLKMWGINITYTGOSTY 349  
 QY 61 ADPFKEFAFSLTETSAATHQINNLNEDSATYFCARRRFGFAWGGTIVSVASISSS 120  
 DB 350 ADPFKEFAFSLTETSAATHQINNLNEDSATYFCARRRFGFAWGGTIVSVASISSS 409  
 QY 121 --SGSSSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIK 178  
 DB 410 GGGSGGGSGSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIK 469  
 QY 179 RLIVATSLDGVKRFSGSRGSDYSLTISLESDPVVYVYCYOYAFPTTGGGNTLLE 238  
 DB 470 RLIVATSLDGVKRFSGSRGSDYSLTISLESDPVVYVYCYOYAFPTTGGGNTLLE 529  
 QY 239 IKRAD 243  
 DB 530 IKRAD 534

RESULT 7  
 AAU04945  
 ID AAU04945 standard; protein; 409 AA.  
 AC AAU04945;  
 XX  
 XX  
 DT 06-AUG-2003 (revised)  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Humanised anti-p185 antibody/IL-2 fusion protein.  
 XX  
 KM Humanised; antibody; p185, 520C9H; interleukin-2, IL-2; immunocombinate;  
 KW cancer; tumour; adenocarcinoma; fusion protein.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Synthetic.  
 OS Chimeric.  
 XX  
 FH Key  
 FT Peptide  
 FT Protein  
 FT Protein  
 FT Protein  
 FT Protein  
 FT Region

Location/Qualifiers  
 1..22  
 /label= Signal\_peptide  
 23..409  
 /label= Mature\_fusion\_protein  
 23..259  
 /label= Humanised\_antibody\_520C9H  
 53..57



Query	Match	Score	DB	Length
1	BIOLVQSPGPELTKPEETVTKISCKASGYTFPANYGMNMKQAPKGLKMMWIMINTYTGQSTY	83.9%	82.9%	60
23	ELGLVQSPGPEVKKPPASVYKISCKASGYTFPANYGMNMKQAPKGLKMMWIMINTYTGQSTY	82.9%	82.9%	60
61	ADDFKFRPAFLSTLSATTAHLQINNLRNEDSATYFCARRGFAYWGQTLVSASISSS	105.5%	105.5%	120

Db	83	ADDFKERTFTLIDTSTAHLEISSLRSDDTLTYFCARRFQRAYWCGGLTVTVS---SGG	139
Oy	121	SGSSSSSGSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEBDGTIKRL	180
Db	140	CGSGGGGSGCGSSDIQMTQSPSSLSASVGDRTLTTCRASQDIGNSLTWLQQRKGTIKRL	199
Oy	161	IYATSSLDGVPKRRPSSGRSGSDYSLTSSLESEDFVTVYCIQYAIFFPTFGGCTNLEIK	240
Db	200	IYATSSLDGVPSSRRSGSGSDYSLTSSLESEDFVTVYCIQYAIFFPTFGGCTNLEIK	259
RESULT 8			
ID	AAU72872		
XX	AAU72872	standard; protein; 499 AA.	
AC	AAU72872;		
XX			
XX	26-FEB-2002	(first entry)	
DT			
XX			
DE	3B10XP4-14	bi-specific single chain Fv.	
XX			
KM	Human; NKGD2; NKGD2 receptor complex; cancer; infectious disease; tumour;		
KM	autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;		
KM	intrabacillary bile duct; pancreas; lung; larynx; breast; uterus; cervix;		
KM	prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;		
KM	sarcoma; leukemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI0;		
KM	helminth; cytotoxic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;		
KM	8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;		
KM	P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10XP4-3; 3B10XP4-14;		
KM	P53 tetramerisation domain; 3B10XP5-2; 3B10XP5-23.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200171005-A2.		
XX			
XX	27-SEP-2001.		
PD			
XX	26-MAR-2001; 2001WO-EP003414.		
PR	24-MAR-2000; 2000EP-00106467.		
XX			
XX	(KUFEE/) KUFER P.		
PI	Kufer P, Riettmueller G, Luterduee R, Borchert K, Kischel R;		
PI	Mayer M, Hofmeister R;		
XX			
DR	WPI: 2002-055119/07.		
XX			
XX	N-PSDB; AAS97146.		
PT			
PT			
PT			
XX			
PS			
XX	Example 5; Fig 16; 114p; English.		
XX			
CC	The invention relates to a multifunctional polypeptide comprising a		
CC	domain with a binding site that specifically recognises an extracellular		
CC	group of the NKGD2 receptor complex and a second domain which functions		
CC	as a receptor or ligand. The polypeptide and its associated		
CC	polynucleotide are used for the preparation of a pharmaceutical		
CC	composition for the treatment of cancer, infections and/or autoimmune		
CC	conditions. The cancer may be a tumour of the head and neck, stomach,		
CC	oesophagus, colon, liver, intrabacillary bile ducts, pancreas, lung,		
CC	larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,		
CC	bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.		
CC	The infectious diseases can be caused by viruses, bacteria, fungi,		
CC	protozoa or helminths. The autoimmune diseases include multiple		
CC	sclerosis, Grave's disease, ankylosing spondylitis, acute anterior		
CC	uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent		
CC	diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and		
CC	autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKGD2		
CC	receptor and the polypeptides of the invention		

```
XX SQ Sequence 499 AA;
Query Match 77.6%; Score 976; DB 5; Length 499;
Best Local Similarity 55.1%; Pred. No. 6.1e-66;
Matches 199; Conservative 13; Mismatches 29; Indels 120; Gaps 1;

QY 1 EIQVQSGPELKKRGETYKISCKASGYTFANYGNMNMKQAPGKGLKMGWINTYTGOSTY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 QVQLQQSGPELKKRGETYKISCKASGYTFANYGNMNMKQAPGKGLKMGWINTYTGOSTY 187
QY 61 ADFKRRPAPSLKETSATTAHLQINNLNEDSATYFCARRRFGFAYWGQGLTVSASISSS 116
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 188 GDFKRRPAPSLKETSATTAHLQINNLNEDSATYFCARRRFGFAYWGQGLTVSASISSS 247
QY 117 -----ISSS 120
Db 248 EVQLLESGGGLVQPGSLKLSCAASGFDFSRHWMNWVROAPGKGLKMGWINTYTGOSTY 307
QY 117 -----ISSS 120
Db 308 TPQLKDFIIRSDNAKNTLYIQMSKVRSEDTALYYCARGAVVAFEDYWGQGLTVVSSSG 367
QY 121 SGSSSSSGSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLQOEPDGTIKRL 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 GGSGGSGSGGSELVMTQSPSSLSASLGERVSLTCRASODIGNSLTWLQOEPDGTIKRL 427
QY 181 IYATSSLDGVPKRFSSGSGSDYSLTISLESDFVYVYCLQYALFPYFGGCTMLEIK 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 428 IYATSSLDGVPKRFSSGSGSDYSLTISLESDFVYVYCLQYALFPYFGGCTMLEIK 487
QY 241 R 241
Db 488 R 488

RESULT 9
AAU04944
ID AAU04944 standard; protein; 267 AA.
XX
AC AAU04944;
XX
DT 06-AUG-2003 (revised)
DT 24-OCT-2001 (first entry)
XX
DE Humanised anti-p185 single chain antibody, 520C9H.
XX
KM Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunocjugate;
KM cancer; tumour; adenocarcinoma.
XX
OS Homo sapiens.
XX
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region /label= CDR
FT /note= "Complementarity determining region"
FT 72..88
FT /label= CDR
FT /note= "Complementarity determining region"
FT 121..126
FT /label= CDR
FT /note= "Complementarity determining region"
FT 138..152
FT /label= CDR
FT /note= "Complementarity determining region"
FT 176..186
FT /label= CDR
FT /note= "Complementarity determining region"
FT 202..208
FT /label= CDR
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FT /note= "Complementarity determining region"
FT 241..249
FT /label= CDR
FT /note= "Complementarity determining region"
FT 250..267
FT /label= Glu_Glu_epitope

XX
XX WO200153354-A2.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001; 2001WO-US001919.
XX
XX 20-JAN-2000; 2000US-0177258P.
XX
XX (CHIR ) CHIRON CORP.
PA (HAMT-) HAMILTON CIVIC HOSPITALS RES DEV INC.
PA (HAMT-) HAMILTON REGIONAL CANCER CENT.
XX
XX Austen R, Kwok CS, Ring DB;
PI
PI WPI; 2001-451904/48.
DR N-PSDB; AAS09507.
XX
XX Novel immunocjugate useful for inhibiting tumor cell growth in vivo
PT comprises a humanized anti-p185 antibody linked to an interleukin-2
PT polypeptide.
XX
XX Claim 7; Fig 9; 74pp; English.
XX
CC The sequence represents a humanised anti-p185 single chain antibody which
CC is linked to a human interleukin-2 (IL-2) molecule to make a fusion
CC protein. The fusion protein (or immunocjugate) is used to inhibit the
CC growth of tumours or cancers particularly those characterised by
CC overexpression of p185 e.g. human adenocarcinomas and malignant and/or
CC benign tumours of the breast, renal system, salivary gland,
CC gastrointestinal tract or gastric tumours. (Updated on 06-AUG-2003 to
CC correct OS field.)
XX
XX SQ Sequence 267 AA;
Query Match 75.6%; Score 950.5; DB 4; Length 267;
Best Local Similarity 71.6%; Pred. No. 2.5e-64;
Matches 174; Conservative 32; Mismatches 34; Indels 3; Gaps 1;

QY 1 EIQVQSGPELKKRGETYKISCKASGYTFANYGNMNMKQAPGKGLKMGWINTYTGOSTY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 EMQLVESGPEVKKPGASVAVKVSCKASGYTFANYGNMNMKQAPGKGLKMGWINTYTGOSTY 82
QY 61 ADFKRRPAPSLKETSATTAHLQINNLNEDSATYFCARRRFGFAYWGQGLTVSASISSS 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 ADFKRRPAPSLKETSATTAHLQINNLNEDSATYFCARRRFGFAYWGQGLTVSASISSS 139
QY 121 SGSSSSSGSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLQOEPDGTIKRL 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 140 GGSGGSGSGGSELVMTQSPSSLSASVGRVITTCRASODIGNSLTWLQOEPDGTIKRL 199
QY 181 IYATSSLDGVPKRFSSGSGSDYSLTISLESDFVYVYCLQYALFPYFGGCTMLEIK 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 200 IYATSSLDGVPKRFSSGSGSDYSLTISLESDFVYVYCLQYALFPYFGGCTMLEIK 259
QY 241 RAD 243
   |||
Db 260 GSE 262

RESULT 10
AAU02278
ID AAU02278 standard; protein; 250 AA.
XX
AC AAU02278;
XX
DT 25-MAR-2003 (revised)
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```

DT 29-OCT-1996 (first entry)
XX 741F8 anti-c-erbB-2 two single chain Fv construct.
DE 741F8 anti-c-erbB-2 two single chain Fv construct.
XX 741F8; anti-c-erbB-2; monoclonal antibody; single chain Fv; sfv;
KW construct; polypeptide linker; C-terminal amino acid sequence;
KW in vivo imaging; drug targeting experiment; homodimer; increased;
KW binding avidity; tissue retention time.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH 122..135
FT /label= linker
FT Peptide 246..250
FT /note="Claimed C-terminal tail to facilitate
FT crosslinking of two sfv polypeptides"
XX US5534254-A.
XX 09-JUL-1996.
PD 07-OCT-1993; 93US-00133804.
XX 06-FEB-1992; 92US-00831967.
XX (CHIR ) CHIRON CORP.
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX Opermann H, Ring DB, Huston JS, Houston LL;
PI WPI: 1996-333194/33.
XX N-PSDB; AAT36878.
DR Compens. contg. antigen-targeting antibody fragment constructs -
XX comprising dimer of single-chain Fv fragments.
XX Claim 25; Col 27-28; 30pp; English.
XX The variable heavy (VH) and variable light (VL) genes of the 741F8 anti-c-
XX -erbB-2 monoclonal antibody (Mab), were isolated from the cDNA of the
XX parental 741F8 hybridoma line. A two single chain Fv (scFv) gene was
XX constructed by connecting the VH and VL genes with a DNA sequence
XX encoding a polypeptide linker. A synthetic DNA duplex encoding the C-
XX terminal amino acid sequence, (Gly)4-Cys was inserted, and the resulting
XX 741F8 anti-c-erbB-2 two sfv inserted into an expression vector. The
XX resulting gene, which encodes the present sequence, was transformed into
XX E. coli, and protein expression induced by the addn. of IPTG to the
XX culture medium. A compen. comprising a carrier and the 2 sfv protein
XX prod. can be used for in vivo imaging, and drug targeting experiments.
XX The 2 sfv protein prod. is a homodimer, in which both fragments target
XX the same antigen, therefore giving greater binding avidity and longer
XX tissue retention times, compared to individual sfv protein prod.
XX fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 250 AA:
SQ
Query Match 72.7%; Score 914; DB 2; Length 250;
Best Local Similarity 71.7%; Pred. No. 1.4e-61;
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;
QY 1 ETQLVOSGBELKPGGTIVKISCKASGYTFTNNGMMVKAPGKGLKMMKMTNTYTGQSTY 60
DB 3 ETQLVOSGBELKPGGTIVKISCKASGYTFTNNGMMVKAPGKGLKMMKMTNTYTGEPY 62
QY 61 ADPFKRFAPFSLTSATTAHLQINNRNDSATYFCARF---GPAVYGGGTIVSVAS 116
DB 63 AEFKGRFAPFSLTSATTAHLQINNRNDSATYFCARF---GPAVYGGGTIVSVAS- 121
QY 117 ISSSSGSSSSSSSSGSDIQMTQSPESLASLGERVSLTCRASQDIGNSLTWLQGPDPGT 176
DB 122 -SSSSGSSSSSSSSSS--SDIVMTQSPKFMSTVGDVRVSIKCKASQDVSTAVAVYQKPGQS 178

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QY 177 IKRLIYATSLSDGVPKRFSGSRGSDYSLTISLSLEDDFVYVYCLQVALFPYTFGCGTN 236
DB 179 PKLLIYVSTRKTRGVPDRFTSGSGSDYTLTISVQABDLAHHYCOQHRYVPTFGGTRK 238
QY 237 LEIKRAD 243
DB 239 LEIKRAD 245
RESULT 11
AAW29261
ID AAW29261 standard; protein; 250 AA.
XX
XX AAW29261;
AC 25-MAR-2003 (revised)
XX 07-JAN-1998 (first entry)
DT Anti-c-erbB-2 single chain antibody 741F8.
XX Adenovirus; E1A; transactivator; transcription activator; stimulate;
KW expression vector; single-chain binding protein; VAI; enhance; PCR;
KW translation; production; immortal; eukaryotic cell; scFv; primer;
KW single-chain antibody fragment; imaging; tumour; breast cancer;
XX ovarian cancer; c-erbB-2 antigen; digoxin intoxication.
XX Synthetic.
XX US5658763-A.
PN 19-AUG-1997.
PD 05-JUN-1995; 95US-00463675.
XX 25-OCT-1993; 93US-00143498.
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX Opermann H, Dorai H;
PI WPI: 1997-424235/39.
XX N-PSDB; AAT91837.
DR Producing single chain binding protein in immortalised eukaryotic cells -
XX which comprise protein coding sequences, a transcription activator and
XX translation promotion sequences, provides high expression at low copy
XX number.
XX Example 2; Col 29-32; 24pp; English.
XX This sequence is a single chain anti-c-erbB-2 antibody (scFv) derived
XX from hybridoma 741F8. The protein product includes a C-terminal tail Gly4
XX -Cys in some constructs. Single-chain antibodies can be produced using a
XX novel method which comprises culturing an immortalised eukaryotic cell
XX having transfected DNA sequences (encoding the protein of interest),
XX integrated into its genome. In particular expression effector vectors
XX containing a non-native reporter DNA (encoding the scFv) and viral
XX sequences to promote transcription and translation (e.g. the adenovirus
XX E1A and VAI genes as shown in AAT91831 and AAT91834 respectively) are
XX used. The scFv that is produced, when properly folded, has a structure
XX with mono- or bi-functional binding activity. The method is especially
XX used to produce single-chain antibody fragments (scFv), e.g. for imaging
XX tumours or delivering therapeutic agents to them, particularly breast and
XX ovarian cancers that express the c-erbB-2 antigen. Other scFv are used in
XX model studies and for treating digoxin intoxication. (Updated on 25-MAR-
XX 2003 to correct PF field.)
XX Sequence 250 AA:
SQ
Query Match 72.7%; Score 914; DB 2; Length 250;
Best Local Similarity 71.7%; Pred. No. 1.4e-61;
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

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Qy      1 EIQLVQSGPELKKPEETVTKISCKASGYTFPANYGNMNMKQAPGKGLKMMGMINTNTYGSTY 60
Db      3 EIQLVQSGPELKKPEETVTKISCKASGYTFINYGNMNMKQAPGKGLKMMGMINTNTGEPY 62
Qy      61 ADDEKERRFAPSLSETATTAHLQINNLRNEDSATYFCARRF----GFAWVGQGLTVSVAS 116
Db      63 AEEFKGRFAPSLSETASTAYLQINNLRNEDPATYFCGRQFTYGGFANWQGLTVYVSA- 121
Qy      117 ISSSSGSSSSGSSGSDIQMTQSPSSLASLGERVSLTCRASODIGNSLTWLOQEPDGT 176
Db      122 -SSSSGSSSSGSSS--SDIWMQSPKFMSTSVGDVRSISCKASQDVSTAVAMVQOKPGQS 178
Qy      177 IKRLIYATSSLDGVPKRFSGSRGSDYSLTISLSESDPFVYYCLOYALFPYTFGGGTN 236
Db      179 PKLLIYMTSTRTHTGVPDRFTGSGSDTYTLTISVQAEIDLALHCCQCHYRVPTFGGGTK 238
Qy      237 LEIKRAD 243
Db      239 LEIKRAD 245

```

## RESULT 12

AAW22400 standard; protein; 250 AA.

AAW22400;

25-MAR-2003 (revised)  
09-OCT-1997 (first entry)

Single chain antibody 741F8 protein sequence.

Production; single-chain; binding protein; antibody; eukaryote; virus;  
transcription activator; promoter; expression; adenovirus; EIA; PCR;  
polymerase chain reaction; amplification; primer; herpes simplex virus;  
thymidine kinase; vector; enhancer; translation; heterologous.

Synthetic.

US5631158-A.

20-MAY-1997.

05-JUN-1995; 95US-00461184.

25-OCT-1993; 93US-00143498.

(CREA-) CREATIVE BIOMOLECULES INC.

Opfermann H, Dorai H;

WPI; 1997-288577/26.

N-PSDB; AAT78879.

Production of cell line for producing single-chain binding protein -  
using construct containing DNA encoding viral transcription activator  
protein.

Example 2; Col 29-32; 24pp; English.

The invention relates to methods of increasing production of a single-  
chain binding protein, especially a single chain antibody, by generating  
eukaryotic cell lines containing DNA encoding either a viral  
transcription activator protein that acts on and stimulates a viral  
promoter controlling the expression of DNA encoding the single-chain  
binding protein, such as the adenovirus Ad2 E1A protein encoded by the  
sequence AAT78873, or an RNA sequence able to promote translation of the  
RNA transcript from the heterologous gene, such as the adenoviral VAI  
gene (AAT78876). The sequence presented here is the amino acid sequence  
of the anti-c-erbB2 single chain antibody 741. The coding sequence was  
constructed by amplifying the variable heavy and light chain genes which  
were then cloned into a PUC vector. For secretion from mammalian cells,  
the sequence is preceded by the signal peptide sequence from the

CC monoclonal antibody 520C9 (AAT78880) or from PacI (AAT78881). (Updated on  
CC 25-MAR-2003 to correct PF field.)  
XX

Sequence 250 AA;

Query Match 72.7%; Score 914; DB 2; Length 250;  
Best Local Similarity 71.7%; Pred. No. 1,4e-61;  
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

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Qy      1 EIQLVQSGPELKKPEETVTKISCKASGYTFPANYGNMNMKQAPGKGLKMMGMINTNTYGSTY 60
Db      3 EIQLVQSGPELKKPEETVTKISCKASGYTFINYGNMNMKQAPGKGLKMMGMINTNTGEPY 62
Qy      61 ADDEKERRFAPSLSETATTAHLQINNLRNEDSATYFCARRF----GFAWVGQGLTVSVAS 116
Db      63 AEEFKGRFAPSLSETASTAYLQINNLRNEDPATYFCGRQFTYGGFANWQGLTVYVSA- 121
Qy      117 ISSSSGSSSSGSSGSDIQMTQSPSSLASLGERVSLTCRASODIGNSLTWLOQEPDGT 176
Db      122 -SSSSGSSSSGSSS--SDIWMQSPKFMSTSVGDVRSISCKASQDVSTAVAMVQOKPGQS 178
Qy      177 IKRLIYATSSLDGVPKRFSGSRGSDYSLTISLSESDPFVYYCLOYALFPYTFGGGTN 236
Db      179 PKLLIYMTSTRTHTGVPDRFTGSGSDTYTLTISVQAEIDLALHCCQCHYRVPTFGGGTK 238
Qy      237 LEIKRAD 243
Db      239 LEIKRAD 245

```

## RESULT 13

AAW47012 standard; protein; 250 AA.

AAW47012;

13-JUL-1998 (first entry)

Single chain binding site molecule (sfv) 741F8.

Single chain binding site molecule 741F8; sfv 741F8; large scale;  
transactivating transcription activator; viral transcription promoter;  
protein production; non-native gene; hard to express gene.

Synthetic.

US5733782-A.

31-MAR-1998.

05-JUN-1995; 95US-00464589.

25-OCT-1993; 93US-00143498.

(CREA-) CREATIVE BIOMOLECULES INC.

Opfermann H, Dorai H;

WPI; 1998-229831/20.

N-PSDB; AAV22398.

Immortalised eukaryotic cell comprising transfected DNA sequences -  
useful for enhanced production of proteins encoded by non native genes.  
Example 2; Col 31-32; 24pp; English.

The present sequence represents single chain binding site molecule (sfv).  
The sequence was expressed to exemplify the invention, which is a method  
for the expression of poorly expressed genes in an immortalised  
eukaryotic cell. This cell contains transfected DNA sequences operatively  
integrated into its genome. The transfected DNA sequences encode a viral  
transcription promoter linked to a non-native reporter sequence encoding  
a single chain binding protein. The promoter is activated by a viral

transcription activator protein. The cell allows the production on a commercial scale of proteins encoded by non-native hard to express genes

Sequence 250 AA;

Query Match 72.7%; Score 914; DB 2; Length 250;  
Best Local Similarity 71.7%; Pred. No. 1.4e-61;  
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

QY 1 EIQLVOSGPELKKPGETVYKISCKASGYTFYFANYGMNMMKQAPGKGLKMMGMINTYTGQSTY 60  
DB 3 EIQLVOSGPELKKPGETVYKISCKASGYTFYFANYGMNMMKQAPGKGLKMMGMINTYTGQSTY 62  
QY 61 ADDEKRFAPFSLTETSAITAHQLQINNLRNEDSATYFCARRF---GPAVWGQGTIVSVSAS 116  
DB 63 AEEFKGRFAPFSLTETSAITAHQLQINNLRNEDSATYFCARRF---GPAVWGQGTIVSVSAS- 121  
QY 117 ISSSSGSSSSGSSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLOQEPDGT 176  
DB 122 -SSSSGSSSSGSSSS--SDIVMTQSPKFMSTVGDVRSISCKASQDVSTAVANYQQKPGQS 178  
QY 177 IKRLIYATSSLDGVPKRFSGSRSGSDYSLTISLSESDPFVYYCLQYAIFFYTFGGGTN 236  
DB 179 PKLLIYMTSTRHTGVPDRFTGSGSGTDYTLTISVQAEIDLALHYCQHRYRVFYTGGGTR 238  
QY 237 LEIKRAD 243  
DB 239 LEIKRAD 245

## RESULT 14

AAW53168  
ID AAW53168 standard; protein; 250 AA.

AC AAW53168;  
DT 16-JUL-1998 (first entry)

DE 741F8 anti-c-erbB-2 sfv' dimeric construct protein sequence.

KW Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer; c-erbB-2;  
tumour; diagnosis.

OS Synthetic.  
MUS Mus sp.

Key Location/Qualifiers  
122..135

FT Peptide /note="linker peptide"

FT Peptide 246..250 /note="Gly4-Cys C-terminal tail"

US5753204-A.

19-MAY-1998.

05-JUN-1995; 95US-00461838.

06-FEB-1992; 92US-00831967.

07-OCT-1993; 93US-00133804.

(CHIR ) CHIRON CORP.

(CREA-) CREATIVE BIOMOLECULES INC.

WPI; 1998-311318/27.

N-PADB; AAV21796.

Imaging of antigens in vivo - using dimers of single-chain antibody Fv fragments.

Example 1; Col 25-28; 30pp; English.

XX This represents the protein sequence of a 741F8 sfv' (single chain Fv) C-terminal Gly4-Cys construct. This was constructed by connecting the Vh and Vh genes with a DNA sequence encoding a 14 residue polypeptide linker. 741F8 is a monoclonal antibody useful in targeting c-erbB-2 antigen. This dimeric construct can be used in the methods of invention of imaging a preselected antigen expressed in a mammal. The methods are used in magnetic resonance imaging of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic constructs have enhanced properties as in vivo targeting agents in comparison with intact monoclonal antibodies or their Fab fragments. The dimeric constructs permit the in vivo targeting of an epitope on an antigen with greater apparent avidity, including greater tumour specificity, tumour localisation and tumour retention properties than that of the Fab fragment having the same CDRS as the construct

Sequence 250 AA;

Query Match 72.7%; Score 914; DB 2; Length 250;  
Best Local Similarity 71.7%; Pred. No. 1.4e-61;  
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

QY 1 EIQLVOSGPELKKPGETVYKISCKASGYTFYFANYGMNMMKQAPGKGLKMMGMINTYTGQSTY 60  
DB 3 EIQLVOSGPELKKPGETVYKISCKASGYTFYFANYGMNMMKQAPGKGLKMMGMINTYTGQSTY 62  
QY 61 ADDEKRFAPFSLTETSAITAHQLQINNLRNEDSATYFCARRF---GPAVWGQGTIVSVSAS 116  
DB 63 AEEFKGRFAPFSLTETSAITAHQLQINNLRNEDSATYFCARRF---GPAVWGQGTIVSVSAS- 121  
QY 117 ISSSSGSSSSGSSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLOQEPDGT 176  
DB 122 -SSSSGSSSSGSSSS--SDIVMTQSPKFMSTVGDVRSISCKASQDVSTAVANYQQKPGQS 178  
QY 177 IKRLIYATSSLDGVPKRFSGSRSGSDYSLTISLSESDPFVYYCLQYAIFFYTFGGGTN 236  
DB 179 PKLLIYMTSTRHTGVPDRFTGSGSGTDYTLTISVQAEIDLALHYCQHRYRVFYTGGGTR 238  
QY 237 LEIKRAD 243  
DB 239 LEIKRAD 245

## RESULT 15

AAW80422  
ID AAW80422 standard; protein; 250 AA.

AC AAW80422;

DT 28-JAN-1999 (first entry)

DE Anti-c-erbB-2 sfv' protein sequence.

KW Anti-c-erbB-2 sfv'; c-erbB-2; antigen; tumour cell; antibody 741F8;  
targeted delivery; antigen-expressing cell.

OS Synthetic.  
HOMO Homo sapiens.

Key Location/Qualifiers  
122..135

FT Peptide /note="linker"

US5837846-A.

17-NOV-1998.

05-JUN-1995; 95US-00461386.

06-FEB-1992; 92US-00831967.

07-OCT-1993; 93US-00133804.

(CREA-) CREATIVE BIOMOLECULES INC.

PA (CHIR ) CHIRON CORP.

XX Oppermann H, Houston LL, Huston JS, Ring DB;

XX WPI: 1999-023541/02.

DR N-PSDB; AAV63397.

XX Nucleic acid encoding single-chain Fv fragment specific for antigens -  
PT and having C-terminal tail for crosslinking to form dimer with improved  
PT pharmacokinetic properties, used to deliver drugs and imaging agents,  
PT especially to tumours.

PS Example 1; Col 27-30; 29pp; English.

XX The present sequence represents an anti-c-erbB-2 sFv'. c-erbB-2 is an  
CC antigen that is overexpressed on the surface of tumour cells. An antibody  
CC designated 741F78 binds c-erbB-2. Variable heavy and light sequences of  
CC antibody 741F8 are connected, together with a linker, to produce the  
CC present single chain Fv gene. Anti-c-erbB-2 sFv' exemplifies the  
CC invention. Dimers of the single chain Fv are used for targeted delivery  
CC of drugs or imaging agents (e.g. cytotoxins, prodrugs or 99m-technetium)  
CC to antigen-expressing cells, particularly for treatment or diagnosis of  
CC tumours (especially of ovary or breast)

XX Sequence 250 AA;

Query Match 72.7%; Score 914; DB 2; Length 250;

Best Local Similarity 71.7%; Pred. No. 1.4e-61;

Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

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QY 1 ETQLVSGPELKKPGRTVTKISCKASGYTFANYGMNMKQAPGKGLKMGMINITYTGOSTY 60
DB 3 ETQLVSGPELKKPGRTVTKISCKASGYTFNYGMNMWKOAPGKGLKMGMININTGSEPTY 62
QY 61 ADDPKERFAFSLKSTATTALQINNLNEDSATYFCARRF---GFAVWGQGLTVSVSAS 116
DB 63 ABEFKRFRFAFSLKSTASTAYLQINNLKNEDEATYFCGRQPIITYGFFANWGQGLTVVSA- 121
QY 117 ISSSSGSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQEPDGT 176
DB 122 -SSSSGSSSSSSGSS--SDIWMTQSPKFMSTSVGDRVVISCKASQDVTAVAWYQQRGQS 178
QY 177 IKRLIYATSLDSGVKRFSGSRSGSDYSLTISLSEDPVYVYCYOYALFPYTFGGGTN 236
DB 179 PKLLIYVSTRHGVDPRTGSGSGTDYTLTLLISVQAEIDLHRYCOQHRYRVPTTFGGGTX 238
QY 237 LRIKRAD 243
DB 239 LRIKRAD 245

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Search completed: April 4, 2005, 15:47:05  
Job time : 488.224 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 358.677 seconds  
(without alignments)  
224.651 Million cell updates/sec

Title: US-09-887-853-6

Perfect score: 1258

Sequence: 1 EQLQVSGPELKKRGETYKI.....YALFFYTRGGTINLEIKRAD 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

1413372

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

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10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*

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19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	100.0	243	9	US-09-887-853-6
2	1258	100.0	243	17	US-10-683-547-6
3	1063.5	84.5	276	9	US-09-766-543-12
4	976	77.6	499	15	US-10-239-656-73
5	950.5	75.6	267	9	US-09-766-543-10
6	914	72.7	250	9	US-09-887-853-2
7	902	71.7	250	17	US-10-683-547-2
8	861.5	68.5	236	17	US-10-879-994-6
9	857.5	68.2	237	9	US-09-924-099-9
10	857.5	68.2	243	9	US-09-924-099-10
11	827	65.7	240	14	US-10-127-890-148
12	827	65.7	240	17	US-10-717-243-148
13	818	65.0	252	15	US-10-239-656-55

14	813.5	64.7	257	15	US-10-239-656-67	Sequence 67, Appl
15	804	63.9	267	14	US-10-071-485-2	Sequence 2, Appl
16	804	63.9	541	14	US-10-071-485-85	Sequence 85, Appl
17	804	63.9	711	14	US-10-071-485-90	Sequence 90, Appl
18	791.5	62.9	240	14	US-10-071-485-91	Sequence 91, Appl
19	786	62.5	505	15	US-10-239-656-79	Sequence 79, Appl
20	782.5	62.2	287	14	US-10-222-026A-37	Sequence 37, Appl
21	782	62.2	503	15	US-10-239-656-77	Sequence 77, Appl
22	779	61.9	235	14	US-10-071-485-93	Sequence 93, Appl
23	766.5	60.9	230	14	US-10-071-485-102	Sequence 102, App
24	766.5	60.9	248	10	US-09-880-748-1104	Sequence 1104, Ap
25	766.5	60.9	248	15	US-10-293-418-1104	Sequence 1104, Ap
26	764	60.7	251	10	US-09-880-748-1921	Sequence 1921, Ap
27	764	60.7	251	15	US-10-293-418-1921	Sequence 1921, Ap
28	764	60.7	503	15	US-10-239-656-75	Sequence 75, Appl
29	762.5	60.6	248	10	US-09-880-748-1446	Sequence 1446, Ap
30	762.5	60.6	248	15	US-10-293-418-1446	Sequence 1446, Ap
31	743.5	59.1	248	10	US-09-880-748-1778	Sequence 1778, Ap
32	743.5	59.1	248	15	US-10-293-418-1778	Sequence 1778, Ap
33	740.5	58.9	250	10	US-09-880-748-932	Sequence 932, App
34	740.5	58.9	250	15	US-10-293-418-932	Sequence 932, App
35	735	58.4	895	16	US-10-296-085A-20	Sequence 20, Appl
36	735	58.4	895	16	US-10-296-085A-19	Sequence 19, Appl
37	735	58.4	895	16	US-10-296-085A-27	Sequence 27, Appl
38	735	58.4	895	17	US-10-496-179-4	Sequence 4, Appl
39	735	58.4	896	16	US-10-296-085A-17	Sequence 17, Appl
40	735	58.4	896	16	US-10-296-085A-18	Sequence 18, Appl
41	735	58.4	896	16	US-10-296-085A-26	Sequence 26, Appl
42	735	58.4	896	17	US-10-496-179-2	Sequence 2, Appl
43	735	58.4	896	17	US-10-496-179-3	Sequence 3, Appl
44	735	58.4	896	17	US-10-496-179-7	Sequence 7, Appl
45	735	58.4	899	16	US-10-296-085A-28	Sequence 28, Appl

## ALIGNMENTS

RESULT 1

US-09-887-853-6

Sequence 6, Application US/09887853

Patent No. US20020168375A1

GENERAL INFORMATION:

APPLICANT: Huston, James S.

Opperman, Hermann

Houston, L. L.

Ring, David B.

TITLE OF INVENTION: BioSynthetic Binding Proteins For Imaging

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSER: Teesta, Hurwitz & Thibault/Patent Department

STREET: Exchange Place, 53 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/887,853

FILING DATE: 21-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/133,804

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Kelley, Robin D.

REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: 2054/22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-887-853-6

Query Match 100.0%; Score 1258; DB 9; Length 243;  
Best Local Similarity 100.0%; Pred. No. 7, 8e-86;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ADPFKEFAPSLFETSAITTAHLQINNLRNEDSATYFCARRFGFAVWGQGLTVSVASISSS 120  
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DB 121 SGSSSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEEDGTIKRL 180  
QY 181 IYATSSLDGVPKRRFGSGRSRGSQSYSLTSSLSBEDFVYVYCLQYAIFFYTFGGGTNLEIK 240  
DB 181 IYATSSLDGVPKRRFGSGRSRGSQSYSLTSSLSBEDFVYVYCLQYAIFFYTFGGGTNLEIK 240  
QY 241 RAD 243  
DB 241 RAD 243

RESULT 2  
US-10-683-547-6  
Sequence 6, Application US/10683547  
Publication No. US20050058638A1  
GENERAL INFORMATION:  
APPLICANT: Huston, J.  
APPLICANT: Houston, L.L.  
APPLICANT: Ring, D.  
APPLICANT: Oppermann, H.  
TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING  
FILE REFERENCE: CIBT-P01-130  
CURRENT APPLICATION NUMBER: US/10/683,547  
CURRENT FILING DATE: 2003-10-10  
PRIOR APPLICATION NUMBER: US/09/558,741  
PRIOR FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: 07/931,967  
PRIOR FILING DATE: 1992-02-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 520C9 sFv  
US-10-683-547-6

Query Match 100.0%; Score 1258; DB 17; Length 243;  
Best Local Similarity 100.0%; Pred. No. 7, 8e-86;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ADPFKEFAPSLFETSAITTAHLQINNLRNEDSATYFCARRFGFAVWGQGLTVSVASISSS 120  
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DB 121 SGSSSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEEDGTIKRL 180  
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QY 241 RAD 243  
DB 241 RAD 243

RESULT 3  
US-09-766-543-12  
Sequence 12, Application US/09766543  
Patent No. US20020041865A1  
GENERAL INFORMATION:  
APPLICANT: Austin, Richard  
APPLICANT: Kwok, Cheuk S.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: METHODS FOR TREATING TUMORS  
FILE REFERENCE: P01679, 002  
CURRENT APPLICATION NUMBER: US/09/766,543  
CURRENT FILING DATE: 2000-01-19  
PRIOR APPLICATION NUMBER: 60/177,258  
PRIOR FILING DATE: 2000-01-20  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 276  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: H520C9sFv plus  
US-09-766-543-12

Query Match 84.5%; Score 1063.5; DB 9; Length 276;  
Best Local Similarity 83.3%; Pred. No. 2, 6e-71;  
Matches 200; Conservative 19; Mismatches 18; Indels 3; Gaps 1;

QY 1 EIQLVSGPELKKRGEYTKISCKASGYTFPANYGNMNMKQAPGKGLKMGWINTYTGOSTY 60  
DB 23 EIQLVSGPEVKKKGASVKISCKASGYTFPANYGNMNMKQAPGKLEMMGWINTYTGOSTY 82  
QY 61 ADPFKEFAPSLFETSAITTAHLQINNLRNEDSATYFCARRFGFAVWGQGLTVSVASISSS 120  
DB 83 ADPFKEFAPSLFETSAITTAHLQINNLRNEDSATYFCARRFGFAVWGQGLTVSVASISSS 120  
QY 121 SGSSSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEEDGTIKRL 180  
DB 140 GSGSGSGSGSGSDIQMTQSPSSLSASVGDVRVTLTCRASQDIGNSLTWLQOEEDGTIKRL 199  
QY 181 IYATSSLDGVPKRRFGSGRSRGSQSYSLTSSLSBEDFVYVYCLQYAIFFYTFGGGTNLEIK 240  
DB 200 IYATSSLDGVPKRRFGSGRSRGSQSYSLTSSLSBEDFVYVYCLQYAIFFYTFGGGTNLEIK 259

RESULT 4  
US-10-239-656-73  
Sequence 73, Application US/10239656  
Publication No. US20040038339A1  
GENERAL INFORMATION:  
APPLICANT: KUPER, PETER  
APPLICANT: RIETHMULLER, GERT  
APPLICANT: LUTTERBUSE, RALF  
APPLICANT: BOSSCHERT, KATRIN  
APPLICANT: KISCHEL, ROMAN  
APPLICANT: MAYER, MONIKA  
APPLICANT: HOMMEISTER, ROBERT



TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE  
FILE REFERENCE: 029976/0106  
CURRENT APPLICATION NUMBER: US/10/239,656  
CURRENT FILING DATE: 2003-03-06  
PRIOR APPLICATION NUMBER: PCT/EP01/03414  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: EP 00106467.4  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 73  
LENGTH: 499  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic 3B10xP4-  
OTHER INFORMATION: 3 bispecific single chain Fv  
US-10-239-656-73

Query Match 77.6%; Score 976; DB 15; Length 499;  
Best Local Similarity 55.1%; Pred. No. 1,6e-64;  
Matches 199; Conservative 13; Mismatches 29; Indels 120; Gaps 1;

QY 1 EIQLVQSGPELKKPGETVTKISCKASGYTFANYGMNMMKQAPGKGLKMMGMINTYTGQSTY 60  
DB 128 QVQLQQSGPELKKPGETVTKISCKASGYTFANYGMNMMKQAPGKGLKMMGMINTYTGQSTY 187  
QY 61 ADFFKERPAFSLSETATTAHLQINLNLRNEDSATYFCARRFGPAYWGQGLTVSVASISS 116  
DB 188 GDFPGRFAFSLSETASTAYLQINLNLRNEDSATYFCARRFGPAYWGQGLTVSVASISS 247  
QY 117 ----- 116  
DB 248 EVQLLESGGGLVQPGSLKSCAASGFDESRYSRWVQAPEGKLEWIGEINPDSSTINY 307  
QY 117 ----- ISSS 120  
DB 308 TPSLKDFPISRDNAKNTIYLQMSKYSRSDTALYCARGAIVAPFPYWGQGLTVSVSSGG 367  
QY 121 SSSSSSSSSSSGSDIQMTQSPPSLSASLGERVSLTCRASQDIGNSLTWMQLQEPDGTIKRL 180  
DB 368 GSGGGGGSGGGSDIQMTQSPPSLSASLGERVSLTCRASQDIGNSLTWMQLQEPDGTIKRL 427  
QY 181 IYATSLDSGVPKRRSGSRGSDYSLTISLSEDFVYVYICQYAIFFPTFGGNTLEIK 240  
DB 428 IYATSLDSGVPKRRSGSRGSDYSLTISLSEDFVYVYICQYAIFFPTFGGNTLEIK 487  
QY 241 R 241  
DB 488 R 488

RESULT 5  
US-09-766-543-10  
Sequence 10, Application US/09766543  
Patent No. US2002004185A1  
GENERAL INFORMATION:  
APPLICANT: Austlin, Richard  
APPLICANT: Kwok, Cheuk S.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: METHODS FOR TREATING TUMORS  
FILE REFERENCE: P01679.002  
CURRENT APPLICATION NUMBER: US/09/766,543  
CURRENT FILING DATE: 2000-01-19  
PRIOR APPLICATION NUMBER: 60/177,258  
PRIOR FILING DATE: 2000-01-20  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 267  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: 520C9  
OTHER INFORMATION: humanized single-chain antibody used in the  
OTHER INFORMATION: IL-2-antibody fusions  
US-09-766-543-10

Query Match 75.6%; Score 950.5; DB 9; Length 267;  
Best Local Similarity 71.6%; Pred. No. 6,4e-63;  
Matches 174; Conservative 32; Mismatches 34; Indels 3; Gaps 1;

QY 1 EIQLVQSGPELKKPGETVTKISCKASGYTFANYGMNMMKQAPGKGLKMMGMINTYTGQSTY 60  
DB 23 EVQLVSGGPEVKKPKGASVYKSCKASGYTFANYGMNMMKQAPGKGLKMMGMINTYTGQSTY 82  
QY 61 ADFFKERPAFSLSETATTAHLQINLNLRNEDSATYFCARRFGPAYWGQGLTVSVASISS 120  
DB 83 ADFFKERPAFSLSETATTAHLQINLNLRNEDSATYFCARRFGPAYWGQGLTVSVASISS 139  
QY 121 SSSSSSSSSGSDIQMTQSPPSLSASLGERVSLTCRASQDIGNSLTWMQLQEPDGTIKRL 180  
DB 140 GSGGGGGSGGGSDIQMTQSPPSLSASVGDRTVITCRASQDIGNSLTWMQLQEPDGTIKRL 199  
QY 181 IYATSLDSGVPKRRSGSRGSDYSLTISLSEDFVYVYICQYAIFFPTFGGNTLEIK 240  
DB 200 IYATSLDSGVPKRRSGSRGSDYSLTISLSEDFVYVYICQYAIFFPTFGGNTLEIK 259  
QY 241 RAD 243  
DB 260 GSE 262

RESULT 6  
US-09-887-853-2  
Sequence 2, Application US/09887853  
Patent No. US20020168375A1  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
Oppermann, Hermann  
Huston, L. L.  
Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Tesca, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/887,853  
FILING DATE: 21-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/133,804  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2  
US-09-887-853-2

Query Match 72.7%; Score 914; DB 9; Length 250;  
Best Local Similarity 71.7%; Pred. No. 3.1e-60;  
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

```
QY 1 EIQLVOSGPELKKPGETYKISCKASGYTFPANYGMNMWKAQPGKGLKMGMINITYGQSTY 60
DB 3 EIQLVOSGPELKKPGETYKISCKASGYTFPANYGMNMWKAQPGKGLKMGMINITYGPEPY 62
QY 61 ADDPKERPAFSLSTATTATLAHQINNLRNEDSATYFCARRF---GPAVWGQGLTVSVSAS 116
DB 63 AEEFKGRPAFSLSTATTATLAHQINNLRNEDSATYFCARRF---GPAVWGQGLTVSVSA- 121
QY 117 ISSSSSSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGT 176
DB 122 -SSSSSSSSSSSSSS--SDIWMQSPKFMSTSVGDVRSISCKASQDVSTAVAMVQOKFGQS 178
QY 177 IKRLIYATSSLDGVPKRRSGSGSDYSLTISLSEDFVYVYCIQVAFPTFGGCTN 236
DB 179 PKLLIYMTSTRHTGVDPDRFTGSGSGTDYTLTISVQAEIDLALHYCOQHRYKVPYTFGGGTYK 238
QY 237 LEIKRAD 243
DB 239 LEIKRAD 245
```

RESULT 7  
US-10-683-547-2  
Sequence 2, Application US/10683547  
Publication No. US20050058638A1

GENERAL INFORMATION:  
APPLICANT: Huston, J.  
APPLICANT: Huston, L.L.  
APPLICANT: Ring, D.  
APPLICANT: Oppermann, H.  
TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING  
FILE REFERENCE: CIBT-P01-130  
CURRENT APPLICATION NUMBER: US/10/683,547  
CURRENT FILING DATE: 2003-10-10  
PRIOR APPLICATION NUMBER: US/09/558,741  
PRIOR FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: 07/831,967  
PRIOR FILING DATE: 1992-02-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 741F8 sfv'  
US-10-683-547-2

Query Match 71.7%; Score 902; DB 17; Length 250;  
Best Local Similarity 70.9%; Pred. No. 2.4e-59;  
Matches 175; Conservative 32; Mismatches 32; Indels 8; Gaps 3;

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QY 1 EIQLVOSGPELKKPGETYKISCKASGYTFPANYGMNMWKAQPGKGLKMGMINITYGQSTY 60
DB 3 EIQLVOSGPELKKPGETYKISCKASGYTFPANYGMNMWKAQPGKGLKMGMINITYGPEPY 62
QY 61 ADDPKERPAFSLSTATTATLAHQINNLRNEDSATYFCARRF---GPAVWGQGLTVSVSAS 116
DB 63 AEEFKGRPAFSLSTATTATLAHQINNLRNEDSATYFCARRF---GPAVWGQGLTVSVSA- 121
QY 117 ISSSSSSSSSSSSSSDQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGT 176
DB 122 -SSSSSSSSSSSSSS--SDIWMQSPKFMSTSVGDVRSISCKASQDVSTAVAMVQOKFGQS 178
```

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QY 177 IKRLIYATSSLDGVPKRRSGSGSDYSLTISLSEDFVYVYCIQVAFPTFGGCTN 236
DB 179 PKLLIYMTSTRHTGVDPDRFTGSGSGTDYTLTISVQAEIDLALHYCOQHRYKVPYTFGGGTYK 238
QY 237 LEIKRAD 243
DB 239 LEIKRAD 245
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RESULT 8  
US-10-879-994-6  
Sequence 6, Application US/10879994  
Publication No. US20050032175A1

GENERAL INFORMATION:  
APPLICANT: Stahl, Neil  
APPLICANT: Yancopoulos, George D.  
APPLICANT: Kato, Margaret  
APPLICANT: Smith, Eric  
TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC METHODS  
FILE REFERENCE: REG 203E2  
CURRENT APPLICATION NUMBER: US/10/879,994  
CURRENT FILING DATE: 2004-06-29  
PRIOR APPLICATION NUMBER: 10/610,452  
PRIOR FILING DATE: 2003-06-30  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 236  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-879-994-6

Query Match 68.5%; Score 861.5; DB 17; Length 236;  
Best Local Similarity 69.7%; Pred. No. 2.3e-56;  
Matches 168; Conservative 26; Mismatches 42; Indels 5; Gaps 2;

```
QY 1 EIQLVOSGPELKKPGETYKISCKASGYTFPANYGMNMWKAQPGKGLKMGMINITYGQSTY 60
DB 1 EIQLVOSGPELKKPGETYKISCKASGYTFPANYGMNMWKAQPGKGLKMGMINITYGPEPY 60
QY 61 ADDPKERPAFSLSTATTATLAHQINNLRNEDSATYFCARRFPAVWGQGLTVSVSASISS 120
DB 61 NQKFRDAXTLTVQDSTTAFAHNLNLTSEDSAVYFCAR--GURFVWGQGLTVSVSA--GG 115
QY 121 SSSSSSSSSSSSDQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIRL 180
DB 116 GSGSGSGSGSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIRL 175
QY 181 IYATSSLDGVPKRRSGSGSDYSLTISLSEDFVYVYCIQVAFPTFGGCTNLEIK 240
DB 176 IYATSSLDGVPKRRSGSGSDYSLTISLSEDFVYVYCIQVAFPTFGGCTNLEIK 235
QY 241 R 241
DB 236 R 236
```

RESULT 9  
US-09-924-099-9  
Sequence 9, Application US/09924099  
Patent No. US20020128450A1

GENERAL INFORMATION:  
APPLICANT: NISHIDA, Yoshihiro  
APPLICANT: OKURA, Takao  
APPLICANT: TANIMOTO, Tadao  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: PEPTIDE  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/924,099  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22  
NUMBER OF SEQ ID NOS: 33  
SEQ ID NO 9  
LENGTH: 237  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially produced peptide in the form of a single  
OTHER INFORMATION: chain  
OTHER INFORMATION: variable region fragment (scfv) which neutralizes IL-18  
US-09-924-099-9

Query Match 68.2%; Score 857.5; DB 9; Length 237;  
Best Local Similarity 69.6%; Pred. No. 4,7e-56;  
Matches 167; Conservative 26; Mismatches 44; Indels 3; Gaps 2;

QY 1 EIQVOSGDELKPKGETVYKISCKASGYTFANYGMNMMKQAPGKGLKMGNTYTGOSTY 60  
DB 1 EIQVOSGDELKPKGASVAVSCASGYSTFDYFIYWKSHGKSLKEMICDIPYNGDTSY 60  
QY 61 ADFFKRFAPSLSTSTTAHLQINLNLRNEDSATYFCARRFPAWYGQGLTVSVASISS 120  
DB 61 NQKFRDKATLVYDQSTTAFHMLNSLTSDSAVYFCAR--GLRFGQGLTVVSAG-GGG 117  
QY 121 SGSSSSGSSSSGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 180  
DB 118 GSGGGGSGGGGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 177  
QY 181 IYATSSLDGVPKRRFSGSRSGSDYSLTSSLESDPFVYVYCCIQYALPYTGGGTNLEIK 240  
DB 178 IYATSSLDGVPKRRFSGSRSGSDYSLTSSLESDPFVYVYCCIQYALPYTGGGTNLEIK 237

## RESULT 10

US-09-924-099-10  
Sequence 10, Application US/09924099  
Patent No. US20020128450A1  
GENERAL INFORMATION:  
APPLICANT: NISHIDA, Yoohihiro  
APPLICANT: OKURA, Takaochi  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: PEPTIDE  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/924,099  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22  
NUMBER OF SEQ ID NOS: 33  
SEQ ID NO 10  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially produced peptide in the form of a single  
OTHER INFORMATION: chain  
OTHER INFORMATION: variable region fragment (scfv) which neutralizes IL-18  
US-09-924-099-10

Query Match 68.2%; Score 857.5; DB 9; Length 243;  
Best Local Similarity 69.6%; Pred. No. 4,8e-56;  
Matches 167; Conservative 26; Mismatches 44; Indels 3; Gaps 2;  
QY 1 EIQVOSGDELKPKGETVYKISCKASGYTFANYGMNMMKQAPGKGLKMGNTYTGOSTY 60  
DB 1 EIQVOSGDELKPKGASVAVSCASGYSTFDYFIYWKSHGKSLKEMICDIPYNGDTSY 60

QY 61 ADFFKRFAPSLSTSTTAHLQINLNLRNEDSATYFCARRFPAWYGQGLTVSVASISS 120  
DB 61 NQKFRDKATLVYDQSTTAFHMLNSLTSDSAVYFCAR--GLRFGQGLTVVSAG-GGG 117  
QY 121 SGSSSSGSSSSGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 180  
DB 118 GSGGGGSGGGGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 177  
QY 181 IYATSSLDGVPKRRFSGSRSGSDYSLTSSLESDPFVYVYCCIQYALPYTGGGTNLEIK 240  
DB 178 IYATSSLDGVPKRRFSGSRSGSDYSLTSSLESDPFVYVYCCIQYALPYTGGGTNLEIK 237

## RESULT 11

US-10-127-890-148  
Sequence 148, Application US/10127890  
Publication No. US20030166196A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
Cartoll, Stephen F.  
Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mcandrews, Heid & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127,890  
FILING DATE: 23-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 148:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 148:  
US-10-127-890-148  
Query Match 65.7%; Score 827; DB 14; Length 240;  
Best Local Similarity 65.8%; Pred. No. 8,8e-54;



```
Db 61 TPLKDKFIIRSDNKNLTLYLQMSKVRSDTALYCARGAVVAPFDYWGQTTVTVS--- 117
Qy 118 SSSSSSSSSSSSSSSSDIOMTQSPSSLASLGERVSLTTRASODIGNSLTWLQOEPDGTI 177
Db 118 SGGGSGGGGSGGGGSELVMTQSPSSLASLGERVSLTTRASODIGNSLTWLQOEPDGTI 177
Qy 178 KLIYATSLDGSVPRKFRSGRSGSDYSLTISLSEDFVYVYCLQYALFPYTFGGGTNL 237
Db 178 KLIYATSLDGSVPRKFRSGRSGSDYSLTISLSEDFVYVYCLQYALFPYTFGGGTNL 237
Qy 238 EIKR 241
Db 238 EIKR 241

RESULT 14
US-10-239-656-67
; Sequence 67, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUPER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOMMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-10 single
; US-10-239-656-67

Query Match 64.7%; Score 813.5; DB 15; Length 257;
Beet Local Similarity 64.7%; Pred. No. 9,5e-53;
Matches 161; Conservative 33; Mismatches 44; Indels 11; Gaps 4;

Qy 1 EIQLV-QSGPELKKPGEYTKISKASGYTFANYGNMNMKQAPGKIKMMKWMINTYTGOST 59
Db 1 EYQLLEQSGAELVKGALVKLSCKASGFYIKDYHVMWQRPBGLEWICWIDPENGNNTI 60
Qy 60 YADDFKRFAPFSLTSATTAAHQLINNLRNEDSATYFCAR--FGFAY----WGQGLVVS 112
Db 61 YDPKFGKASITADYTSNTAYLQLSSLTSEDTAAAYCASFYYSYRFDVWGQGTVT 120
Qy 113 VVASISSSSSSSSSSGSDIOMTQSPSSLASLGERVSLTTRASODIGNSLTWLQOE 172
Db 121 VS--SGGGSGGGGSGGGSELVMTQSPSSLASLGERVSLTTRASODIGNSLTWLQOE 177
Qy 173 PDGTTIKRLIYATSLDGSVPRKFRSGRSGSDYSLTISLSEDFVYVYCLQYALFPYTFG 232
Db 178 PDGTTIKRLIYATSLDGSVPRKFRSGRSGSDYSLTISLSEDFVYVYCLQYALFPYTFG 237
Qy 233 GGTNLEIKR 241
Db 238 GGTNLEIKR 246
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```
RESULT 15
US-10-071-485-2
; Sequence 2, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic
; US-10-071-485-2

Query Match 63.9%; Score 804; DB 14; Length 267;
Beet Local Similarity 63.8%; Pred. No. 5e-52;
Matches 155; Conservative 32; Mismatches 50; Indels 6; Gaps 3;

Qy 1 EIQLVQSGPELKKPGEYTKISKASGYTFANYGNMNMKQAPGKIKMMKWMINTYTGOSTY 60
Db 23 QVQLVQSGSELKRPASVXISKASGYTFITDYGMMVMVQAPQGKIKMMKWMINTYTGESTY 82
Qy 61 ADDEFKRFAPFSLTSATTAAHQLINNLRNEDSATYFCAR--FGFAYWGQGLVVSASIS 118
Db 83 VDDFKRFVPSLDTVSAAVYLQISSLKAEDTATYFCARRGFYAMDYWGQGTVTVS---S 139
Qy 119 SSSSSSSSSSSSGSDIOMTQSPSSLASLGERVSLTTRASODIGNSLTWLQOEPDGTIK 178
Db 140 GGGGSGGGGSGGGSDIYLTQSPATMSASPERVTLTCSASSSI-SYMFVWHQRPQSGPR 198
Qy 179 RLIVATSLDGSVPRKFRSGRSGSDYSLTISLSEDFVYVYCLQYALFPYTFGGGTNLE 238
Db 199 LIIYDTSLMAGVPRKFRSGSGSGTISYSLTISRMEPEDATYTFCHOSSSYPTTFGGGTNLE 258
Qy 239 IKR 241
Db 259 IKR 261
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Search completed: April 4, 2005, 16:42:42  
Job time : 359.677 secs

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## OM protein - protein search, using sw model

Run on: April 4, 2005, 15:32:36 ; Search time 87.7284 seconds

(without alignments)  
266.512 Million cell updates/sec

Title: US-09-887-853-6

Perfect score: 1258  
Sequence: 1 EIQLVQSGPELKKRGFTYKI.....YAIFFYTRGGGNLEIKRAD 243Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summariesDatabase : PIR 79:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	591.5	47.0	268	2	A56446 Ig heavy chain V r
2	571	45.4	249	2	S41374 single chain Fv an
3	521.5	41.5	146	4	S33905 Ig heavy chain pre
4	520.5	41.4	120	2	B42848 16 mb heavy chain
5	517	41.1	136	2	S35759 BHD9D10 protein -
6	512	40.7	117	2	S32190 Ig heavy chain V r
7	510	40.5	119	2	A53285 Ig heavy chain V a
8	508	40.4	130	1	KVMSM4 Ig kappa chain pre
9	507	40.3	118	2	S19967 Ig heavy chain V r
10	505.5	40.2	115	2	S19968 Ig heavy chain V r
11	503.5	40.0	118	2	S37204 Ig heavy chain V r
12	501	39.8	233	2	UC5322 p53 specific singl
13	498	39.6	106	2	PL0260 Ig kappa chain V r
14	498	39.6	106	2	PL0259 Ig kappa chain V r
15	497.5	39.5	109	2	S26325 Ig heavy chain V r
16	497	39.5	113	2	B36259 Ig heavy chain V r
17	492	39.1	119	2	H45722 anti-glycoprotein
18	489	38.9	124	2	PH1404 Ig heavy chain V r
19	488	38.8	117	2	S32187 Ig heavy chain V r
20	487.5	38.8	115	2	S19965 Ig heavy chain V r
21	485.5	38.6	114	2	D32967 Ig heavy chain V r
22	475.5	37.8	114	2	C32967 Ig heavy chain V r
23	468.5	37.3	118	2	A32530 Ig heavy chain V r
24	468	37.2	106	2	PL0262 Ig kappa chain V r
25	466.5	37.1	139	2	PH1225 Ig heavy chain pre
26	462.5	36.8	120	2	S19963 Ig heavy chain V r
27	462	36.7	119	2	B32530 Ig heavy chain V r
28	456	36.2	105	2	S24765 Ig heavy chain V r
29	453	36.0	114	2	PL0256 Ig heavy chain V r

30	447	35.5	108	4	B47271 nitrophenyl phosph
31	444	35.3	105	2	S24764 Ig heavy chain V r
32	433.5	34.5	101	2	D24672 Ig heavy chain V r
33	432	34.3	98	2	PH1062 Ig light chain V r
34	431	34.3	105	2	S24766 Ig heavy chain V r
35	423.5	33.7	120	2	S26789 Ig heavy chain V r
36	418.5	33.3	144	2	B30502 Ig heavy chain V r
37	418	33.2	134	2	S21916 Ig heavy chain V r
38	415	33.0	99	2	S26326 Ig heavy chain V r
39	415	33.0	105	2	S24763 Ig heavy chain V r
40	415	33.0	142	2	S19245 Ig heavy chain pre
41	413	32.8	88	2	PL0261 Ig kappa chain V r
42	412.5	32.8	93	2	C24672 Ig heavy chain V r
43	405	32.2	131	2	S26792 Ig heavy chain V r
44	404	32.1	129	2	D32513 Ig kappa chain pre
45	400	31.8	115	2	JU0080 Ig kappa chain pre

## ALIGNMENTS

## RESULT 1

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/c)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
C/Accession: A56446  
R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical  
A/Reference number: A56446; MUID:9522983; PMID:7713873  
A/Accession: A56446  
A/Status: Preliminary  
A/Molecule type: mRNA  
A/Residues: 1-268 <TAN>  
A/Cross-references: GB:U20617  
C/Keywords: heterotetramer; immunoglobulin

Query Match 47.0%; Score 591.5; DB 2; Length 268;  
Best Local Similarity 47.8%; Pred. No. 3e-35;  
Matches 117; Conservative 46; Mismatches 75; Indels 7; Gaps 3;

QY	1	EIQLVQSGPELKKRGFTYKICKSGYTFANVGMNMQAPKQKXMGWITTYGQSY	60
DB	3	QVKIQESGAELVKKPQASVSLCTTSGFNIKDTYHVMVQRPQGLEWIGRIAPANGITKY	62
QY	61	ADDFKRFAPSLTETSATTAHLQINNLRNEDSATYFCARRFGFA--YWGQGLVSVSASI	117
DB	63	DPKFGKATIAADTSNNTAYQLDLSLTSEDTNAYVCASYILRYENMGQITTVS---	119
QY	118	SSSSGSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQSPDGTI	177
DB	120	SGGGSGGGSDGGGSDIELTQSPAIMSASLGERKWTSCRASSV-NFIYWYQKSDASP	178
QY	178	KRLIYATSSLDGVPKRRSGSGSDYSLTSSLSBDFVYYCYQVAFPTTFGGGTTU	237
DB	179	KLVVYITSLPVPARFARPSGSGNSYSLSISMGEDAAATYCCQAFSSPTFGSTWL	238
QY	238	EIKRA 242	
DB	239	EIKRS 243	

## RESULT 2

S41374  
single chain Fv antibody - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C/Accession: S41374  
R/Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A/Description: Construction and functional characterization of a single chain Fv antibody  
A/Reference number: S41374







RESULT 10  
S19968  
Ig heavy chain V region (M-T408) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S19968  
R.Weissenhorn, W.; Rietmuller, G.; Weiss, E.M.; Rieber, E.P.  
Submitted to the EMBL Data Library, March 1992  
A/Description: Structural characterization of CD4 mAb.  
A/Reference number: S19963  
A/Accession: S19968  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-115 <MKT>  
A/Cross-references: UNIPROT:Q921A6, EMBL:X65089  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotetramer; Immunoglobulin  
F/10-93/Domain: Immunoglobulin homology <IMM>

Query Match 40.2%; Score 505.5; DB 2; Length 115;  
Best Local Similarity 80.9%; Pred. No. 1.6e-29;  
Matches 93; Conservative 8; Mismatches 9; Indels 5; Gaps 1;  
QY 6 QSGPELKKPGETVTKISCKASGYTFPANYGMNMMKQAPGKGLKMGWINTYTGSGTYADDFK 65  
DB 1 QSGPELKTPTGETVTKISCKASGYTFPANYGMNMMKQAPGKGLKMGWINTYTGSGTYADDFK 60  
QY 66 ERPAFSLSTSTTAHLOINNLRNEDSATYPCAR----RFQFAYWGQGLTVSVSA 115  
DB 61 GRPAFSLSTSTAYVLOINNLKNEDTAAYFCARGPYRSPYWGQGLTVTVSS 115

RESULT 11  
S37204  
Ig heavy chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Jun-2000  
C/Accession: S37204  
R.Fischer, R.; Voess, A.; Hunziker, W.; Stierhof, V.D.; Kreuzaler, F.  
Submitted to the EMBL Data Library, August 1993  
A/Description: Production and cloning of TMV-specific monoclonal antibodies.  
A/Reference number: S37200  
A/Accession: S37204  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-118 <FIS>  
A/Cross-references: EMBL:X74589; NID:g402599; PIDD:CA52666.1; PID:g1333981  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
F/15-98/Domain: Immunoglobulin homology <IMM>

Query Match 40.0%; Score 503.5; DB 2; Length 118;  
Best Local Similarity 79.8%; Pred. No. 2.2e-29;  
Matches 95; Conservative 12; Mismatches 7; Indels 5; Gaps 2;  
QY 1 EILVDSGPELKKPGETVTKISCKASGYTFPANYGMNMMKQAPGKGLKMGWINTYTGSGTY 60  
DB 1 QILVDSGPELKKPGETVTKISCKASGYTFIDYSMHVWQVPGKGLKMGWINTETGEAKY 60  
QY 61 ADDFKRPAFSLSTSTTAHLOINNLRNEDSATYPCARPG---FAYWGQGLTVSVSA 115  
DB 61 ADDFKRPAFSLSTSTAYVLOINNLKNEDTAAYFCA-RWGSAMFPYWGQGLTVSA 118

RESULT 12  
JCS322  
p53 specific single-chain antibody Fab421 - human  
C/Species: Homo sapiens (man)  
C/Date: 15-May-1997 #sequence\_revision 15-May-1997 #text\_change 18-Jul-1997  
C/Accession: JCS322  
R.Jannot, C.B.; Hynes, N.E.  
Biochem. Biophys. Res. Commun. 230, 242-246, 1997  
A/Title: Characterization of scFv-421, a single-chain antibody targeted to p53.  
A/Reference number: JCS322; MUID:97168950; PMID:9016757

A/Accession: JCS322  
A/Molecule type: mRNA  
A/Residues: 1-233 <JAN>  
A/Experimental source: hybridoma cell  
C/Comment: This protein specifically binds the tumor suppressor protein p53. It restores  
Query Match 39.8%; Score 501; DB 2; Length 233;  
Best Local Similarity 43.3%; Pred. No. 7.3e-29;  
Matches 103; Conservative 46; Mismatches 79; Indels 10; Gaps 4;  
QY 6 QSGPELKKPGETVTKISCKASGYTFPANYGMNMMKQAPGKGLKMGWINTYTGSGTYADDFK 65  
DB 2 ESGAEIVRSQASVKISCTSGFNIDYHWHWKKRPEQLEIGRIDPENGADMTRSSG 61  
QY 66 ERPAFSLSTSTTAHLOINNLRNEDSATYPCARRRPFAYWGQGLTVSVSAISSSSGSS 125  
DB 62 VAAITMTADTSTAYVLOISLTSLEDYAVYTC--NAGMDYWGQGLTVSVS---SGGSGSG 116  
QY 126 SGSSSSGSDIQMTGSPSSLSASLGERVSLTCRASQDIGNS----LTWLOQEPDGTIKRLI 181  
DB 117 RASGGGSDIELTQSPASLAVSLGQRAVISCRAKSVSTSGYSVHMMNQKPDGPPRLII 176  
QY 182 YATSSLDGVPKRFSGSSGSDYSLTSSLSSEDFVYTCIQYAIFFYTFGGTNLEI 239  
DB 177 YIVSNLESQVPAFRFGSSGSDFTLNIHPVEEDAAATYTC-QHIRELTRSGGTLEI 233

RESULT 13  
PL0260  
Ig kappa chain V region (anti-DNA, DP1VK) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
C/Accession: PL0260  
R.Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.  
J. Exp. Med. 171, 265-297, 1990  
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n  
A/Reference number: PL0231; MUID:90111618; PMID:2104919  
A/Accession: PL0260  
A/Molecule type: mRNA  
A/Residues: 1-106 <SHL>  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotetramer; Immunoglobulin  
F/1-23/Region: framework 1  
F/16-90/Domain: immunoglobulin homology <IMM>  
F/24-34/Region: complementarity-determining 1  
F/35-49/Region: framework 2  
F/50-56/Region: complementarity-determining 2  
F/57-88/Region: framework 3  
F/89-97/Region: complementarity-determining 3  
F/98-106/Region: framework 4

Query Match 39.6%; Score 498; DB 2; Length 106;  
Best Local Similarity 93.4%; Pred. No. 4.9e-29;  
Matches 99; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 134 DIQMTGSPSSLSASLGERVSLTCRASQDIGNSLTWIQOEPDGTIKRLIATSSLDGVRK 193  
DB 1 DIQMTGSPSSLSASLGERVSLTCRASQDIGNSLTWIQOEPDGTIKRLIATSSLDGVRK 60  
QY 194 RFGSGRSGSDYSLTSSLSSEDFVYTCIQYAIFFYTFGGTNLEI 239  
DB 61 RFGSGRSGSDYSLTSSLSSEDFVYTCIQYASPTTFGGTNLEI 106

RESULT 14  
PL0259  
Ig kappa chain V region (anti-DNA, DP1VK) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
C/Accession: PL0259  
R.Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.  
J. Exp. Med. 171, 265-297, 1990  
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n

A:Reference number: PL0231; MUID:90111618; PMID:2104919  
A:Accession: PL0259  
A:Molecule type: mRNA  
A:Residues: 1-106 <SHL>  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:1-23/Region: framework 1  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:24-34/Region: complementarity-determining 1  
F:35-49/Region: framework 2  
F:50-56/Region: complementarity-determining 2  
F:57-88/Region: framework 3  
F:89-97/Region: complementarity-determining 3  
F:98-106/Region: framework 4

Query Match 39.6%; Score 498; DB 2; Length 106;  
Best Local Similarity 93.4%; Pred. No. 4.9e-29;  
Matches 99; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 134 DIQMTQSPSSLSASISGERYSITCRASQDIGNSLTWIQEPPDGIKRLIYVTSISLDSGVPK 193  
DB 1 DIQMTQSPSSLSASISGERYSITCRASQDIGNSLTWIQEPPDGIKRLIYVTSISLDSGVPK 60

QY 194 RFGSGRSGSDYSLTISLSEEDFVVYVYCIQYAIFFPYTFGGTNIET 239  
DB 61 RFGSGRSGSDYSLTISLSEEDFVDYCIQYATSPWTFGGTNIET 106

RESULT 15  
S26325  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S26325  
R:Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e  
A:Reference number: S26309; MUID:91341421; PMID:1908510  
A:Accession: S26325  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-109 <STA>  
A:Cross-references: UNIPROT:Q921A6; EMBL:X59210; NID:952080; PUD:91334043  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:5-88/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 497.5; DB 2; Length 109;  
Best Local Similarity 85.3%; Pred. No. 5.5e-29;  
Matches 93; Conservative 7; Mismatches 4; Indels 5; Gaps 2;

QY 11 LKKPGETVXISCKASGYTFANYGMNMKQAPGKGLKMGMINITYTQSTYADDFKRFAPF 70  
DB 1 LKKPGETVXISCKASGYTFANYGMNMVKAAPGKGLKMGMINITYTGEPTYADDFKRFAPF 60

QY 71 SLETSATTHLQINLNINRSDSATYFCAR---RF-GFATWGQGITVSVS 114  
DB 61 SLETSASTAYLQINLNKEDMATYFCARPAYRYDGFATWGQGITVTVS 109

Search completed: April 4, 2005, 15:57:59  
Job time : 89.7284 secs

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Db 236 LELKRA 241

## RESULT 2

065ZC8 PRELIMINARY; PRT; 244 AA.

AC 065ZC8; 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DE Single-chain Fv (Fragment).  
 Name=scfv;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97362799; PubMed=9219263;  
 RA Kontermann R.E., Wing M.G., Winter G.;  
 RT "Complement recruitment using bispecific diabodies."  
 RL Nat. Biotechnol. 15:629-631(1997).  
 DR EMBL; Y13057; CA73500.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG\_2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGv; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 FT NON TER 1  
 FT 244  
 SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 58.6%; Score 737.5; DB 2; Length 244;  
 Best Local Similarity 55.5%; Pred. No. 6,1e-51;  
 Matches 137; Conservative 47; Mismatches 54; Indels 9; Gaps 2;

QY 1 EIQLVSGPELKKRGKGVTKISCKASGYTFANYGMNMMKQAFGKGLKMGWINTYTGSTY 60  
 Db 1 QVQLVSGGAVKRPDSVKVSCKASGTFPSDHYHWVRQAPGGGLMWMGMDIPNDTRF 60  
 QY 61 ADDPKERFAPSLTSAATTAHLQINNLNEDSATYFCARR-----FGFAYWGQGLVSVS 114  
 Db 61 AGRFQGVVTWTRDPTISAAVMEVSRRLRSDPLVAYYCARFGTSAIYGMWQGLVTVIS 120  
 QY 115 ASISSSSSSSSSSSSSSDIQTQSPSSLSASLGERVSLTCRASODIGNSLTWLQEPD 174  
 Db 121 ---SGGGSGGGSGGGSDIQTQSPSTLSASIGDRVITCRASGEGYHWLAWYQKPKG 177  
 QY 175 GTRKRLIYATSSLDGCVPKRFGSGRSDYSLTISLSEDFVYVYCLQYALFPYTFGGG 234  
 Db 178 KAKPKFLIYKASSLSASAPRFSGSGTPTLTLSLQPDPAFYTCQQYSNYPFLFGGG 237  
 QY 235 TNLKTR 241  
 Db 238 TKLEIKR 244

## RESULT 3

065ZC9 PRELIMINARY; PRT; 240 AA.

AC 065ZC9; 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DE Single-chain Fv (Fragment).  
 Name=scfv;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C1q/7;  
 RX MEDLINE=97362799; PubMed=9219263;  
 RA Kontermann R.E., Wing M.G., Winter G.;  
 RT "Complement recruitment using bispecific diabodies."  
 RL Nat. Biotechnol. 15:629-631(1997).  
 DR EMBL; Y13056; CA73499.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGv; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 FT NON TER 1  
 FT 240  
 SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 54.9%; Score 690.5; DB 2; Length 240;  
 Best Local Similarity 55.6%; Pred. No. 3.4e-47;  
 Matches 135; Conservative 40; Mismatches 63; Indels 5; Gaps 2;

QY 1 EIQLVSGPELKKRGKGVTKISCKASGYTFANYGMNMMKQAFGKGLKMGWINTYTGSTY 60  
 Db 1 QVQLVSGGGLVQPGSLRLSCASGTFSSYGMHWVRQAPGKGLFWAVAYSYGSKNYY 60  
 QY 61 ADDPKERFAPSLTSAATTAHLQINNLNEDSATYFCARRFGFAY--WGQGLVSVASIS 118  
 Db 61 ADSVKGRTTISRDSKNTLYQMSLRAEDYVAYYCARMDGSDLPWGKGLTVS--S 117  
 QY 119 SSSGSSSSSSSSSSSDIQTQSPSSLSASLGERVSLTCRASODIGNSLTWLQEPDGTIK 178  
 Db 118 GGGSGGGSGGGSDIQTQSPSTLSASIGDRVITCRASGEGYHWLAWYQKPKAPK 177  
 QY 179 RLIVATSLDGVGPKRFGSGRSDYSLTISLSEDFVYVYCLQYALFPYTFGGGNTLE 238  
 Db 178 LLIKYASSLSAPRFSGSGGTPTLTSSLQPDPAFYTCQQYSNYPFLFGGKTLK 237  
 QY 239 IKR 241  
 Db 238 IKR 240

## RESULT 4

0925S1 PRELIMINARY; PRT; 218 AA.

AC 0925S1; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE MRS (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX PubMed=11819679;  
 RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
 Su C.;  
 RT "Mechanism of exogenous nucleic acids and their precursors improving  
 the repair of intestinal epithelium after irradiation in mice."  
 RL World J. Gastroenterol. 6:709-717(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA Cui D., Zeng G., Yan X., Li X., Su C.;  
 RT "Cloning of mouse genes related to repairing of intestinal epithelium  
 of the irradiated mice by treatment with the intestinal RNA of mice of  
 the same strain."  
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).

DR EMBL: AF240168; AAK43733.1; -.  
DR HSSP: P01665; 10N2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON TER 218 218  
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 52.5%; Score 661; DB 2; Length 218;  
Best Local Similarity 58.9%; Pred. No. 6.9e-45;  
Matches 129; Conservative 32; Mismatches 48; Indels 10; Gaps 3;

QY 1 EIQLVQSGPELKKPEETVYKISCKASGYTFANYGMNMWKAQPKGLKMKMGINITYGQSTY 60  
DB 3 QYKQOQSGPELKKPEETVYKISCKASGYTTTGMQWQVQMPKGLKMKMGINITHSGVPRX 62  
QY 61 ADDEKRFAPFSLTETATTAHLQINNLRNEDSATYFCAR--RFGPAYWQGTLYVSASIS 117  
DB 63 AEEFKGRFAPFSLTETATTAHLQINNLKNEDTATYFCMRWDYDGFAYWQGTLYTVS--- 119  
QY 118 SSSSGSSSSSGSDIQMTQSPSLSASLGERVSLTCRASQDIGN---SLTWLQOEP 173  
DB 120 SGGSGSGSGSGSDIVLTQSPASLAVSLQORATISCRASGSVDNIGISFMNWFQKRP 179  
QY 174 DGTIKRLIYATSLDSGVPKRFRSGSRGSDYSLTISLSE 212  
DB 180 GQPKLLIYAAKQSGSGVPAAGLLASGSGTDFSLNTYPMK 218

## RESULT 5

Q7TQM2 PRELIMINARY; PRT; 243 AA.

AC 07TQM2; PRELIMINARY; PRT; 243 AA.  
DT 01-OCT-2003 (TRENBLrel. 25, Created)  
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE SCFV 6H8 protein (Fragment).  
CN Name=SCFV 6H8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Balb/C.  
RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;  
RA Peter J.C., Ettehchari P., Billiald P., Wallukat G., Hoebeke J.;  
RT "scfv single chain antibody variable fragment as inverse agonist for  
RT the beta-2 adrenergic receptor";  
RL J. Biol. Chem. 278:36740-36747(2003).  
DR EMBL; AJ574851; CAB00495.1; -.  
DR HSSP; P01751; 1A6W.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
FT NON TER 1 1  
SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DCFAF76 CRC64;

Query Match 50.6%; Score 636.5; DB 2; Length 243;  
Best Local Similarity 52.3%; Pred. No. 7.1e-43;  
Matches 126; Conservative 43; Mismatches 67; Indels 5; Gaps 3;

QY 1 EIQLVQSGPELKKPEETVYKISCKASGYTFANYGMNMWKAQPKGLKMKMGINITYGQSTY 60  
DB 1 QVQLQOQSGSELVTPASVTLSCASGYTFYTMHMHVXKQHQGLQLEWIGINITYPGSGITNY 60  
QY 61 ADDEKRFAPFSLTETATTAHLQINNLRNEDSATYFCAR--RFGPAYWQGTLYVSASIS 119  
DB 61 DEKFKRKGILVDTSSSTAYMHLSSLASDSAVYTCARGRGIDVWGAQTTTLTVS---SG 117  
QY 120 SSSSGSSSSSGSDIQMTQSPSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIR 179  
DB 118 GGGSGSGSGSGSDIQMTQSSSSPSVSLGDRVTITCKASEDIYNRLANYQKQPKGNAPRL 177

QY 160 LIYATSLDSGVPKRFRSGSRGSDYSLTISLSEDPFVYVYCLQYALPPTFGGNTLEI 239  
DB 178 LISGATSLTETVPSRFRSGSGKDYTLTSLQEDVATYVCOQY-WSTRTRGGKXLEI 236  
QY 240 K 240  
DB 237 K 237

## RESULT 6

QOQYFO PRELIMINARY; PRT; 298 AA.

AC 09QYFO; PRELIMINARY; PRT; 298 AA.  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE CN 8 single chain antibody.  
GN Name=CN 8 scFv;  
OS synthetic construct.  
OC other sequences; artificial sequences.  
OX NCBI\_TaxId=32630;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20183931; PubMed=10706631; DOI=10.1073/pnas.050582197;  
RA Shiohara N., Demura T., Fukuda H.;  
RT "Isolation of a vascular cell wall-specific monoclonal antibody  
RT recognizing a cell polarity by using a phase display subtraction  
RT method";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).  
DR EMBL; AB036341; BAA88633.1; -.  
DR PIR; A33933; A33933.  
DR PIR; S19112; S19112.  
DR HSSP; P01820; 1A7O.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 50.6%; Score 636; DB 2; Length 298;  
Best Local Similarity 51.4%; Pred. No. 1e-42;  
Matches 126; Conservative 42; Mismatches 71; Indels 6; Gaps 3;

QY 1 EIQLVQSGPELKKPEETVYKISCKASGYTFANYGMNMWKAQPKGLKMKMGINITYGQSTY 60  
DB 40 QYKQOQSGGGLVYKPGSGLKLSCAASGSDFSRYMGMVVRQAPKGLQLEWIGINIPDSSTINY 99  
QY 61 ADDEKRFAPFSLTETATTAHLQINNLRNEDSATYFCAR--RFG--AYWGQGTLYVSASIS 117  
DB 100 TPSLDKFTISRDNKNTLYLQMSKVRSEDTALVYTCARASYGHSAYWQGTTLTVS--- 156  
QY 118 SSSSGSSSSSGSDIQMTQSPSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTI 177  
DB 157 SGGSGSGSGSGSDIELTQSPASLSASVETVITTCRASGNHNYLAWQKQKGRSP 216  
QY 178 KRLIYATSLDSGVPKRFRSGSRGSDYSLTISLSEDPFVYVYCLQYALPPTFGGNTL 237  
DB 217 QLVVNAKTLADGVPSRFRSGSGGTQYSLKINSIQPEDFGSYCQHFMTTPYTFGGGTYL 276  
QY 238 EIKRA 242  
DB 277 EIKRA 281

## RESULT 7

Q65ZL2 PRELIMINARY; PRT; 487 AA.

AC 065ZL2; PRELIMINARY; PRT; 487 AA.  
DT 25-OCT-2004 (TRENBLrel. 28, Created)  
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
DE FV/M4.

GN Name=M4-IFN-<tau>;  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCB1\_TaxID=10095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96272580; PubMed=8688499;  
RA Qi Y., Xiang J.,  
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric  
antibody secreted from myeloma cells."  
RL Hum. Antibodies Hybridomas 6:161-166 (1995).  
DR EMBL; S82493; AAB37424.2; -  
DR InterPro; IPR003599; IG\_1.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003597; IG\_G1.  
DR InterPro; IPR003598; IG\_G2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF07654; C1-set; 2.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00409; Ig; 3.  
DR SMART; SM00407; IgC1; 2.  
DR SMART; SM00408; IgC2; 2.  
DR SMART; SM00406; IgV; 2.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
SQ SEQUENCE 487 AA; 53578 MW; C7EAB69F30555504 CRC64;

Query Match 50.0%; Score 629.5; DB 2; Length 487;  
Best Local Similarity 50.8%; Pred. No. 6,1e-42;  
Matches 122; Conservative 46; Mismatches 67; Indels 5; Gaps 2;

QY 1 EIQVOSGPELKKPGETVTKISCKASGYTPANYGMNMKQAPGKGLKMGWINTYTGSTY 60  
DB 20 QVQLQQSGDDELVPKSGSVKISCKASGYTFDTHAIHWAKKPEQGLIGWIGTSPGNDIRY 79  
QY 61 ADDPKERFAFSLTETSAITTAHLQINNLRNEDSATYFCARRRFGAYWGQGLTVSVASIS 120  
DB 80 NEKFKKATLTAKSSSTAMQNLSTSESNAYFCRRY-YHWQGGTTLTG---SGG 134  
QY 121 SGSSSSGSSSGSDIQMTQSPSSLASLGERVSLTCRASODIGNSLTWLGQEBDGTIKEL 180  
DB 135 GSGGGGSGSGSGSRIMQTSPLSYSGVELVITTCRASENIYSNLAWYQKQKSGSPQL 194  
QY 181 IVATSLDGVPRFSGSRSGSDYSLTISLSEDPVVVYCCQYALFPTTREGGTLLEIK 240  
DB 195 VYATNLADGVPRFSGSGSGDTQYSLKINSLSQEDFGSYCOHFWGTPTTFCGTRLEIK 254

## RESULT 8

Q6KB05 PRELIMINARY; PRT; 255 AA.  
AC O6KB05;  
DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
DE SCFV B8E5 protein (Fragment).  
GN Name=scfv B8E5;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCB1\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Balb/c;  
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ746180; CAG34081.1; -  
DR HSSP; F01837; 1KCR.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig\_1like.

DR InterPro; IPR003596; Ig\_V.  
DR SMART; SM00409; Ig; 2.  
DR SMART; SM00406; IgV; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
FT NON TER 1  
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 49.2%; Score 618.5; DB 2; Length 255;  
Best Local Similarity 48.0%; Pred. No. 2,1e-41;  
Matches 121; Conservative 46; Mismatches 70; Indels 15; Gaps 3;

QY 1 EIQVOSGPELKKPGETVTKISCKASGYTPANYGMNMKQAPGKGLKMGWINTYTGSTY 60  
DB 1 QVQLQQSGDDELVPKSGSVKISCKASGYTFDTHAIHWAKKPEQGLIGWIGTSPGNDIRY 79  
QY 61 ADDPKERFAFSLTETSAITTAHLQINNLRNEDSATYFCARRF-----GPAVWGQGLTVS 114  
DB 61 PDSVKGRTTISRDNKNTLYLQMSLSKSEDTAMVCAHINRYRGAFDYGQGLTTLVS 120  
QY 115 ASISSSGSSSGSSGSDIQMTQSPSSLASLGERVSLTCRASODIGNS-----LTW 168  
DB 121 ---SGGGSGSGSGSDIYVMAQSPSSLVSAGEKIVMSCKSQSLNSRNQNYLAW 177  
QY 169 LQGPEDGTIKRLIYATSLDGVPRFSGSRSGSDYSLTISLSEDPVVVYCCQYALF 228  
DB 178 YQKRGQSPKLLIYASTRESGVPDRFTGSGSGDTFTLTSSVQAEHLAVYCONDSHP 237  
QY 229 YTFGGGTMLEIK 240  
DB 238 LTFGAGTLEIK 249

## RESULT 9

Q65ZQ7 PRELIMINARY; PRT; 248 AA.  
ID Q65ZQ7;  
AC Q65ZQ7;  
DT 25-OCT-2004 (T-EMBLrel. 28, Created)  
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)  
DE B3 (Fv)-PE40 (Fragment).  
GN Name=B3 (Fv)-PE40;  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCB1\_TaxID=10095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92020904; PubMed=1924323;  
RA Brinkmann U., Pal L.H., FitzGerald D.J., Williamson M., Pastan I.,  
RT "B3 (Fv)-PE38DEL, a single-chain immunotoxin that causes complete  
regression of a human carcinoma in mice."  
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620 (1991).  
DR EMBL; S57990; AAB19971.2; -  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 2.  
DR SMART; SM00406; IgV; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
FT NON TER 248  
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 46.9%; Score 590; DB 2; Length 248;  
Best Local Similarity 48.2%; Pred. No. 3,8e-39;  
Matches 120; Conservative 45; Mismatches 72; Indels 12; Gaps 4;

QY 1 EIQVOSGPELKKPGETVTKISCKASGYTPANYGMNMKQAPGKGLKMGWINTYTGSTY 60  
DB 2 DVKLVESGGGLVPGGSLKISCKASGYTFSDYIMYWRQPEKRLMVAIISNDSSAAV 61  
QY 61 ADDPKERFAFSLTETSAITTAHLQINNLRNEDSATYFCARRF---PAYWGQGLTVSVAS 116



DB 62 SDTVKGRFTIRSDNANRLTYLQMSRLKSEDTAIVSCARGLANCAWPAWV3QGTLYTVS-- 119

QY 117 ISSSSSSSSSSSSSDIQMTQSPSSLSALGERSLTCRASODI-----GMS-LTWLQO 171

DB 120 -GGGGSSGGGGGGSDVLTMTQSPLSVSLGDDQASISCRSSQIIVHSINGTYLEWYIQ 178

QY 172 EDDGTIKRLIYVTSLSLSDSGSRGSGSDYSLTISLSLESEDFVYVYCLQYAIIPYTE 231

DB 179 KCGQSPKLLIYVSNRFSGVPRFSSGSGDTPLTKISRVENADLVGYVLCFGSHVPTTF 238

QY 232 GGGTNLEIK 240

DB 239 GSGTKLEIK 247

RESULT 10

ID 099LA6 PRELIMINARY; PRT; 484 AA.

AC 099LA6; 01-JUN-2001 (TRENBLrel. 17, Created)

DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxId=10090;

RP SEQUENCE FROM N.A.

RC STRAIN-mix FVB/N; TISSUE=Mammary tumor;

RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/dnae.242603399;

RA Straube R.L., Felgould E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D., Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K., Hopfner R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diacchione L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Teshnyuk S., Carninci P., Prange C., Rabe S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J., Roark S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., White M., Helton E., Kerteman M., Madan A.C., Rodrigues S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN-mix FVB/N; TISSUE=Mammary tumor;

RA Straube R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC003495; AA003495.1; -.

DR PIR; F33932; F33932.

DR PIR; S19963; S19963.

DR HSSP; P01810; 2F8J.

DR InterPro; IPR003597; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF07654; Cl-sec; 2.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG\_LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.

KW Hypothetical protein.

SEQUENCE 484 AA; 52567 MW; 8EAEAF9BCF582FA CRC64;

Query Match 41.1%; Score 517; DB 2; Length 484;

Best Local Similarity 37.4%; Pred. No. 5.8e-33;

Matches 123; Conservative 32; Mismatches 52; Indels 122; Gaps 9;

QY 1 EIQLYVSGPELKKPPTVYKISCKASGYTPAAYGAMMKAPKGLKMMKINITYTQSTY 60

DB 20 QIQLYVSGPELKKPPTVYKISCKASGYTPDYSMMHVAKAPGKGLMMKQVNIETESVY 79

QY 61 ADDPKERFAPFLETSAATTAHLQINNLRNEDSAATYFCAR-----FGFAYWGQGTIVSVS 114

DB 80 ADDPKERFAPFLETSAATTAHLQINNLKNDTATYFCARADYDYDIYAMDYWGQGTIVSVS 139

QY 115 A-----SISS-----SGSSSSSSSSSDIQMTQSPSSLSA 146

DB 140 SESARNPTIYPLTPPALSSDPVITGLIDYFPGSGTMVTVWCKSGKIDITTVFPALAS 199

QY 147 S----- 147

DB 200 GGRYTWSSQQLTPAVECPGESEVKCSVQHDSPVDELVNCGAPRPPRTIIPSCOPSLS 259

QY 148 -----LGERVSLTCRAS---QDIGNSLTWLQOEP-----DGTIKRLI-----YAT 184

DB 260 LQRPALIEDLLSGSDASITTLNGLRNPEGAVFTW---EFTGKDAVQKAVQNSCGCTSY 316

QY 185 SSLDSGVPRKFRFSRSGSDYSLTISLES 213

DB 317 SSVLPQCAERMN---SGASFCTVTHPES 342

RESULT 11

ID KVS6 MOUSE STANDARD; PRT; 130 AA.

AC P01639; P01640;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ig kappa chain V-V region MOPC 41 precursor.

DE Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxId=10090;

RP SEQUENCE FROM N.A.

RC MEDLINE=79221900; PubMed=111146;

RX Seidman J.G., Max E.B., Leder P.; "A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation."

RT Nature 280:370-375(1979).

RL [2]

RP SEQUENCE OF 1-33.

RX MEDLINE=77148916; PubMed=403522;

RA Buretein Y., Schechter I.; "Amino acid sequence of the NH2-terminal extra piece segments of the RT precursors of mouse immunoglobulin lambda1-type and kappa-type light RT chains."

RT Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).

RL [3]

RP SEQUENCE OF 23-130.

RX MEDLINE=67056897; PubMed=4162931;

RA Gray W.R., Dreyer W.J., Hood L.; "Mechanism of antibody synthesis: size differences between mouse kappa RT chains."

RT Science 155:465-467(1967).

CC -I- MISCELLANEOUS: This precursor was synthesized in a cell-free system directed by mRNA isolated from myeloma polybromes.

CC -I- MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR; A33211; KVM5M4.

DR HSSP; P01594; IJVS.

DR InterPro; IPR003596; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG\_LIKE; 1.

DR Bence-Jones protein; Direct protein sequencing;

KW Immunoglobulin V region; Signal.

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FT SIGNAL 1 22
FT CHAIN 23 130 Ig kappa chain V-V region M06C 41.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 23 45 Complementarity-determining-1.
FT DOMAIN 46 56 Framework-2.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 119 Complementarity-determining-3.
FT DOMAIN 120 128 Framework-4.
FT DISULFID 120 128 By similarity.
FT VARIANT 45 110 Missing (in 25% of the molecules).
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 14311 MW; 58FE0FE71D5F1BEC CRC64;

Query Match 40.4%; Score 508; DB 1; Length 130;
Best Local Similarity 93.5%; Pred. No. 6e-33;
Matches 101; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 134 DIQMTQSPSLASLGERVSLTCSRASQDIGNSLTWLQOEPDGTIKRLIYATSSLDGVPK 193
Db 23 DIQMTQSPSLASLGERVSLTCSRASQDIGNSLTWLQOEPDGTIKRLIYATSSLDGVPK 82

Qy 194 RFGSGRSGSDYSLTISLSEDEFDVYVYCLQYALFPYTFGGGTLEIKR 241
Db 83 RFGSGRSGSDYSLTISLSEDEFDVYVYCLQYASPTFGGTLEIKR 130

RESULT 12
Q925S9 PRELIMINARY; PRT; 127 AA.
ID 0925S9;
AC 0925S9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=99306687; PubMed=10380019;
RA Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
RA Foon K.A., Chatterjee S.K.;
RT "Construction and characterization of a chimeric fusion protein
RT consisting of an anti-idiotypic antibody mimicking a breast cancer-
RT associated antigen and the cytokine GM-CSF."
RL Hydridoma 18:193-202(1999).
DR EMBL; AF124721; AK55120.1; -.
DR HSSP; P01594; 1UVS.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 127 127
SQ SEQUENCE 127 AA; 13794 MW; 13F61BBB8B981FAS CRC64;

Query Match 39.1%; Score 492; DB 2; Length 127;
Best Local Similarity 91.6%; Pred. No. 1.1e-31;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 134 DIQMTQSPSLASLGERVSLTCSRASQDIGNSLTWLQOEPDGTIKRLIYATSSLDGVPK 193
Db 21 DIQMTQSPSLASLGERVSLTCSRASQDIGNSLTWLQOEPDGTIKRLIYATSSLDGVPK 80

Qy 194 RFGSGRSGSDYSLTISLSEDEFDVYVYCLQYALFPYTFGGGTLEIKR 240
Db 81 RFGSGRSGSDYSLTISLSEDEFDVYVYCLQYASPTFGGTLEIKR 127

RESULT 13
Q683Y7 PRELIMINARY; PRT; 116 AA.
ID 0683Y7;
AC 0683Y7;
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DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Immunoglobulin heavy chain variable region (Fragment).
GN Name=IGHV;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Phalipon A., Costachel C., Thunizat A., Nato F.;
RT "Anti-11popsaccharide antibodies protective against Shigella
RT flexneri 2a infection recognize an immunodominant serotype-specific
RT determinant on the O-antigen."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ784033; CAH04483.1; -.
DR InterPro; IPR003599; IG_.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12863 MW; 5EC11AD02B911952 CRC64;

Query Match 37.4%; Score 470.5; DB 2; Length 116;
Best Local Similarity 75.0%; Pred. No. 5.2e-30;
Matches 87; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

Qy 1 EIQVQSGDELKPEETIKSCASGYTPANYGMNMMQARGLKMMGWINTYGGSTY 60
Db 1 EIVQLQSGPOLKTPETIEISCKASVYTLTDYSLHWVQGGKGLRMWGWINTETGEPA 60

Qy 61 ADDFERAFSLSTATTAAHQQNNLRNEDSATYFCA-RRGFAYWGGGTLVSVA 115
Db 61 ADDFERAFSLSTATTAAHQQNNLRNEDTRATYFCAGIRYDGAIVGGGTLVVA 116

RESULT 14
Q65ZL3 PRELIMINARY; PRT; 140 AA.
ID 065ZL3;
AC 065ZL3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tg10H (Fragment).
GN Name=Tg10H;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96269537; PubMed=8699031; DOI=10.1016/0022-1759(96)00043-9;
RA Noel D., Bernardi T., Navarro-Reulon I., Marin M., Martineto D.P.,
RA Ducancel F., Mani J.C., Pau B., Plechaczky M., Blard-Plechaczky M.;
RT "Analysis of the individual contributions of immunoglobulin heavy and
RT light chains to the binding of antigen using cell transfection and
RT plasmom resonance analysis."
RL J. Immunol. Methods 193:177-187(1996).
DR EMBL; S82492; AAB37434.2; -.
DR InterPro; IPR003599; IG_.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15302 MW; 7BFE237F3D965FA3 CRC64;
```

```
Query Match      36.4%; Score 458.5; DB 2; Length 140;
Best Local Similarity 69.4%; Pred. No. 5.9e-29;
Matches 84; Conservative 18; Mismatches 14; Indels 5; Gaps 1;

QY 1 ETLVQVSGPELKKPGETVYISCKASGYTPFANYGMNMWKOAPGKGLKMMGINTYTGOSTY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 QTHLVQSGPELKKPGETVYISCKASGYTPSYGLTWVIOSPGKDLKMMGINTPFGVPTY 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADDPKERAFSLSETSATTAHLQINNLRNDSATYFCARRFGFA----YMGQGLVSVSA 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 ADDPKGRFAPSLDTSSTAYLQIDNLKNEDTATYFCSTRGCFITTAIDTWGQGLSVSS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 116 S 116
   :
DB 140 A 140

RESULT 15
ID 09JUL79 PRELIMINARY; PRT; 102 AA.
AC 09JUL79;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A.CA;
RX MEDLINE=20448942; PubMed=10992488;
RX DOI=10.1128/JAI.68.10.5803-5808.2000;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206027; AAF69325.1; -.
DR HSSP; P01751; INOB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 102
SQ SEQUENCE 102 AA; 11543 MW; E590C292093F6711 CRC64;

Query Match      34.7%; Score 436; DB 2; Length 102;
Best Local Similarity 79.4%; Pred. No. 2.5e-27;
Matches 81; Conservative 10; Mismatches 9; Indels 2; Gaps 1;

QY 16 ETVKISCKASGYTPFANYGMNMWKOAPGKGLKMMGINTYTGOSTYADDPFERFAPSLSTS 75
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 ETVKISCKASGYTPFDYSGMWVWKOAPGKGLKMMGWINTETGEPTVADDPKGRFAPSLSTS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 76 ATTAHLQINNLRNDSATYFCARRFG--PAYMGQGLVSVSA 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ASTAFLQINNLRNEDTATYFCVKNWASWFAIWGQGLVTVSA 102
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Search completed: April 4, 2005, 15:56:00  
Job time : 412.693 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: April 4, 2005, 15:19:49 ; Search time 29.9521 seconds  
(without alignments)  
193.690 Million cell updates/sec

Title: US-09-887-853-8  
Perfect score: 66  
Sequence: 1 SSSSSSSSSSSSSSG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq.16dec04:\*

- 1: geneeqp19808:\*
- 2: geneeqp19908:\*
- 3: geneeqp20008:\*
- 4: geneeqp20018:\*
- 5: geneeqp20028:\*
- 6: geneeqp20038:\*
- 7: geneeqp20038a:\*
- 8: geneeqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	66	100.0	15	2	AAR39572
2	66	100.0	15	3	AA90828
3	66	100.0	15	4	AAU0868
4	66	100.0	15	4	AAU04949
5	66	100.0	15	7	ABW00718
6	66	100.0	15	8	ADN60232
7	66	100.0	15	8	ADR38601
8	66	100.0	17	3	AA67939
9	66	100.0	17	3	AA617004
10	66	100.0	17	6	ADB24918
11	66	100.0	17	7	ADB24915
12	66	100.0	17	7	ABU10017
13	66	100.0	17	8	ADQ28276
14	66	100.0	31	3	AA15670
15	66	100.0	31	5	AAQ22543
16	66	100.0	31	5	ABP97039
17	66	100.0	31	8	ADN60233
18	66	100.0	34	5	ABP56042
19	66	100.0	243	2	AAW02280
20	66	100.0	243	2	AAW53170
21	66	100.0	243	2	AAW80424
22	66	100.0	243	7	ABW00716
23	66	100.0	246	2	AAAR39569
24	66	100.0	261	2	AAAR44230
25	66	100.0	433	2	AAAR91073

26	66	100.0	433	2	AAW07598	AAW07598 Basic fib
27	66	100.0	433	3	AA90459	AA90459 bGCF/ser
28	66	100.0	433	7	ADG34725	ADG34725 Human bG
29	66	100.0	433	7	ADH92143	ADH92143 Fibroblas
30	62	93.9	246	2	AAAR27245	AAAR27245 Light (VL
31	62	93.9	246	2	AAAR44229	AAAR44229 Chimeric
32	62	93.9	252	2	AAW02279	AAW02279 26-10 ant
33	62	93.9	252	2	AAW53169	AAW53169 26-10 ant
34	62	93.9	252	2	AAW80423	AAW80423 Anti-digo
35	62	93.9	252	7	ABW00715	ABW00715 26-10 bFv
36	62	93.9	367	2	AAAR27244	AAAR27244 Sequence
37	62	93.9	471	2	AAAR27246	AAAR27246 Sequence
38	60	90.9	15	5	AAAG80185	AAAG80185 Fusion co
39	60	90.9	15	6	ABU08677	ABU08677 Human sin
40	60	90.9	250	2	AAW02278	AAW02278 741F8 ant
41	60	90.9	250	2	AAW29261	AAW29261 Anti-c-er
42	60	90.9	250	2	AAW22400	AAW22400 Single ch
43	60	90.9	250	2	AAW47012	AAW47012 Single ch
44	60	90.9	250	2	AAW53168	AAW53168 741F8 ant
45	60	90.9	250	2	AAW80422	AAW80422 Anti-c-er

## ALIGNMENTS

RESULT 1  
AAR39572  
ID AAR39572 standard; protein; 15 AA.  
XX  
AC AAR39572;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-FEB-1994 (first entry)  
XX  
DE Sequence of a new linker.  
XX  
KW Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;  
KW biosynthetic single polypeptide chain binding site.  
XX  
OS Synthetic.  
XX  
PN WO9316185-A2.  
XX  
PD 19-AUG-1993.  
XX  
PF 05-FEB-1993; 93WO-US001055.  
XX  
PR 06-FEB-1992; 92US-00831967.  
XX  
PA (CREA-) CREATIVE BIOMOLECULES INC.  
PA (CETU) CETUS ONCOLOGY CORP.  
XX  
PI Huston JS, Huston LL, Ring DB, Oppermann H;  
XX MPI. 1993-272889/34.  
DR N-PSDB; AAQ46087.  
XX  
PT New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for  
PT imaging or treating breast or ovarian cancer etc.  
XX  
PS Example; Page 70; 87pp; English.  
XX  
XX c-erbB-2 refers to a protein antigen expressed on the surface of tumour  
XX cells, such as breast and ovarian tumour cells, which is an approx.  
XX 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about  
XX 5.3 (see AAQ46083, AAR39568). A single chain Fv (bFv) is a covalently  
XX linked VH-VL heterodimer which is expressed from a gene fusion including  
XX VH- and VL- encoding genes connected by a peptide-encoding linker. Such  
XX linker sequences are set forth in AA residues 116-135 in AAR39569, which  
XX includes part of the 16 AA linker sequences in AAR39572. Using AAQ46084  
XX produced having a binding affinity for a c-erbB-2 related antigen.  
XX (Updated on 25-MAR-2003 to correct PN field.)

XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 66; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSSSSSSSSSSSSG 15  
DB 1 SSSSSSSSSSSSSG 15

## RESULT 2

AA90828  
ID AA90828 standard; peptide; 15 AA.

XX  
AC AA90828;

XX  
DT 29-AUG-2000 (first entry)

XX  
DE Linker amino acid sequence SEQ ID NO:31.

XX  
KW Antigen binding site; immunoglobulin; cancer antigen; immunological;  
KW antibody; tumour; human; mucin; cancer; cytosolic; hybridoma;  
KW specific binding assay; affinity purification; drug targeting;  
KW toxin targeting; imaging; genetic; therapeutic.

XX  
OS Synthetic.

XX  
PN US6054561-A.

XX  
PD 25-APR-2000.

XX  
PF 07-JUN-1995; 95US-00483749.

XX  
PR 08-FEB-1984; 84US-00577976.

XX  
PR 11-JAN-1985; 85US-00690750.

XX  
PR 21-MAR-1986; 86US-00842476.

XX  
PR 08-MAY-1988; 88US-00190778.

XX  
PR 11-AUG-1994; 94US-00288981.

XX  
PA (CHIR) CHIRON CORP.

XX  
PI Ring DB;

XX  
DR WPI; 2000-338508/29.

XX  
XX Monoclonal antibody capable of binding to human breast cancer antigen

XX  
PT useful for affinity purification, drug or toxin targeting, imaging, and

XX  
PT treating cancer.

XX  
PS Disclosure; Col 77; 57pp; English.

XX  
XX The present invention describes a monoclonal antibody (Mab) (I) that

XX  
CC binds to a human breast cancer antigen that is also bound by Mab 454C11

XX  
CC and 520C9 (produced hybridoma ATCC HB9484 and HB8696, respectively). Also

XX  
CC described is a hybridoma that produces (I). (I) is useful in specific

XX  
CC binding assays, affinity purification, drug or toxin targeting, imaging,

XX  
CC and genetic or immunological therapeutics for various cancers. The

XX  
CC present sequence represents a linker amino acid sequence which is used in

XX  
CC the exemplification of the present invention

XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 66; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSSSSSSSSSSSSG 15  
DB 1 SSSSSSSSSSSSSG 15

RESULT 3  
AAU08688  
ID AAU08688 standard; peptide; 15 AA.

XX  
AC AAU08688;

XX  
DT 18-DEC-2001 (first entry)

XX  
DE Antibody L19-Fibronectin-2 (IL-2) fusion protein amino acid linker.

XX  
KW Angiogenesis; extracellular matrix; ED-B domain; fibronectin; lesion;

XX  
KW IL-2; doxorubicin; interleukin-12; interferon-gamma; IL-12; IFN-gamma;

XX  
KW Tumour Necrosis Factor alpha; TNF alpha; tissue factor protein; angiotensin;

XX  
KW electrochemical potential; tumour; cancer; rheumatoid arthritis;

XX  
KW diabetic retinopathy; age related muscular degeneration; cytosolic;

XX  
KW antirheumatic; antiarthritic; antidiabetic; ophthalmological.

XX  
OS Synthetic.

XX  
PN WO200162298-A2.

XX  
PD 30-AUG-2001.

XX  
PF 22-FEB-2001; 2001WO-IB000382.

XX  
PR 24-FEB-2000; 2000US-0184767P.

XX  
PR 21-DEC-2000; 2000US-0257192P.

XX  
PA (PHIL-) PHILGEN SRL.

XX  
PI Zardi L, Neri D, Carmemolla B, Nilsson F, Tarli L, Borsi L;

XX  
PI Halin C;

XX  
DR WPI; 2001-596713/67.

XX  
XX Novel conjugate for treating lesions, comprises a specific binding member

XX  
PT specific for extra-cellular matrix component present in lesions, and a

XX  
PT molecule that exerts biocidal/cytotoxic effect on target cells in

XX  
PT lesions.

XX  
XX Example 1; Page 30; 88pp; English.

XX  
PS The invention relates to a conjugate comprising a molecule that exerts a

XX  
XX biocidal or cytotoxic effect on target cells in lesions of pathological

XX  
CC angiogenesis and an antibody (L19) directed against an extracellular

XX  
CC matrix component (the ED-B domain of fibronectin) which is present in the

XX  
CC lesions. Examples of biocidal or cytotoxic molecules include fibronectin-

XX  
CC 2 (IL-2), doxorubicin, interleukin-12 (IL-12), interferon-gamma (IFN-

XX  
CC gamma), Tumour Necrosis Factor alpha (TNF alpha) tissue factor protein.

XX  
CC These proteins may interact with a membrane-bound receptor on the target

XX  
CC cell or perturb the electrochemical potential of the cell membrane. The

XX  
CC treatable disorders include tumours, rheumatoid arthritis, diabetic

XX  
CC retinopathy, age related muscular degeneration and angiotensin. This

XX  
CC sequence represents an amino acid linker encoded by a PCR primer used in

XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 66; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSSSSSSSSSSSSG 15  
DB 1 SSSSSSSSSSSSSG 15

## RESULT 4

AAU04949  
ID AAU04949 standard; peptide; 15 AA.

XX  
AC AAU04949;

XX  
XX

DT 24-OCT-2001 (first entry)  
 XX  
 DE Humanised anti-p185 antibody/IL-2 fusion protein, linker peptide #2.  
 XX  
 KW Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunoconjugate;  
 KW cancer; tumour; adenocarcinoma; fusion protein.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200153354-A2.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 19-JAN-2001; 2001WO-US0001919.  
 XX  
 PR 20-JAN-2000; 2000US-0177258P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 PA (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.  
 PA (HAMI-) HAMILTON REGIONAL CANCER CENT.  
 XX  
 PI Austen R, Kwok CS, Ring DB;  
 XX  
 PI WPI: 2001-451904/48.  
 DR  
 XX  
 PT Novel immunoconjugate useful for inhibiting tumor cell growth in vivo  
 PT comprises a humanized anti-p185 antibody linked to an interleukin-2  
 PT polypeptide.  
 PS  
 XX  
 PS Disclosure; Page 16; 74pp; English.  
 XX  
 CC The sequence represents a linker peptide used to make a humanised anti-  
 CC p185 (520C9) single chain antibody/human interleukin-2 (IL-2) fusion  
 CC protein. The fusion protein (or immunoconjugate) is used to inhibit the  
 CC growth of tumours or cancers particularly those characterized by  
 CC overexpression of p185 e.g. human adenocarcinomas and malignant and/or  
 CC benign tumours of the breast, renal system, salivary gland,  
 CC gastrointestinal tract or gastric tumours  
 CC  
 SQ Sequence 15 AA;  
 XX

Query Match 100.0%; Score 66; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSSSGSSSG 15  
 |||||  
 DB 1 SSSSGSSSSSGSSSG 15

RESULT 5  
 ABM00718  
 ID ABM00718 standard; peptide; 15 AA.  
 XX  
 AC ABM00718;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Linker #2, peptide used in the invention.  
 XX  
 DE Cell proliferation; cytotoxic agent; drug targeting.  
 XX  
 OS Unidentified.  
 XX  
 PN US2002168375-A1.  
 XX  
 PD 14-NOV-2002.  
 XX  
 PF 21-JUN-2001; 2001US-00887853.  
 XX  
 PR 06-FEB-1992; 92US-00831967.  
 PR 07-OCT-1993; 93US-00133804.  
 PR 05-JUN-1995; 95US-00462641.

PR 26-APR-2000; 2000US-00558741.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Huston JS, Houston LL, Ring DB, Oppermann H;  
 XX  
 DR WPI: 2003-765156/72.  
 XX  
 PT Novel binding protein formulation for targeting epitope on antigen in  
 PT mammal, comprising dimeric biosynthetic construct having conformation  
 PT permitting binding of antigen by binding site of each polypeptide chain.  
 XX  
 PS Disclosure; Page 2; 30pp; English.  
 XX  
 CC The invention relates to a binding protein formulation for targeting an  
 CC epitope on an antigen expressed in mammal. The formulation comprises of  
 CC dimeric biosynthetic construct having conformation permitting binding of  
 CC antigen by binding site of each polypeptide chain. The invention is  
 CC useful for imaging a preselected antigen in a mammal expressing the  
 CC antigen. It is also useful for targeting drugs that inhibit cell  
 CC proliferation and cytotoxic agents that kill cells. The present sequence  
 CC is a linker peptide used in the invention  
 CC  
 SQ Sequence 15 AA;  
 XX

Query Match 100.0%; Score 66; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSSSGSSSG 15  
 |||||  
 DB 1 SSSSGSSSSSGSSSG 15

RESULT 6  
 ADN60232  
 ID ADN60232 standard; protein; 15 AA.  
 XX  
 AC ADN60232;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Linker peptide.  
 XX  
 KW linker; self-assembled monolayer.  
 XX  
 OS Synthetic.  
 XX  
 PN US6723517-B1.  
 XX  
 PD 20-APR-2004.  
 XX  
 PF 02-JUN-1999; 99US-00324258.  
 XX  
 PR 02-JUN-1998; 98US-0087766P.  
 XX  
 PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.  
 XX  
 PI Bamdad CC;  
 XX  
 DR WPI: 2004-386879/36.  
 XX  
 PT Determining of distance between binding sites on target molecule  
 PT comprises contacting target molecule with self-assembled monolayer, and  
 PT identifying controlled geometry with lowest density.  
 XX  
 PS Disclosure; SEQ ID NO 18; 37pp; English.  
 XX  
 CC The invention relates to a method for determination of distance between  
 CC binding sites on a target molecule, involving contacting the target  
 CC molecule with a self-assembled monolayer comprising binding moieties  
 CC immobilised with respect to each other in controlled geometries,  
 CC identifying the controlled geometry with lowest density of immobilised

CC binding moieties that elicits a jump in affinity for the target molecule,  
 CC and determining the distance between immobilised binding moieties in the  
 CC controlled geometry with the lowest density to determine the distance  
 CC between binding sites on the target molecule. The self-assembled  
 CC monolayers incorporate thiol species capable of displaying a binding  
 CC moiety to the target molecule, and inert spacer thiol component. Changes  
 CC in binding affinity are correlated to a density of the thiol species.  
 CC Statistical calculations are applied to a critical binding moiety density  
 CC and thiol packing dimensions to determine a probable distance between the  
 CC immobilised binding moieties. Extracted distance information is used in  
 CC rational design of multi-valent drugs. Surface plasmon resonance is used  
 CC to measure binding affinities between immobilized binding moieties and  
 CC target molecule in solution. The target molecule is a protein complex.  
 CC The thio species is a nitrilo tri-acetic acid terminated thiol. The  
 CC present sequence represents a linker peptide which was used with  
 CC immobilised binding moieties in the method of the invention.

SQ Sequence 15 AA;  
 Query Match 100.0%; Score 66; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 0.012;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSSSSSSSG 15  
 |||||  
 Db 1 SSSSGSSSSSSSSSG 15

RESULT 7  
 ADR38601  
 ID ADR38601 standard; peptide; 15 AA.  
 AC ADR38601;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Anti-botulinum neurotoxin antibody associated linker #3.  
 XX  
 KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
 KM BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KW toxin neutralisation; botulinum neurotoxin poisoning; linker.  
 XX  
 OS Synthetic.  
 XX  
 PN US2004175385-A1.  
 XX  
 PD 09-SEP-2004.  
 XX  
 PF 01-AUG-2003; 2003US-00632706.  
 XX  
 PR 31-AUG-1998; 98US-00144886.  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX  
 PA (REGC ) UNITV CALIFORNIA.  
 XX  
 PI Marks JD, Amersdorfer P;  
 PI  
 DR WPI; 2004-652009/63.  
 XX  
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.  
 XX  
 PS Disclosure; SEQ ID NO 3; 110pp; English.  
 XX  
 CC The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (i) binds to and neutralises botulinum neurotoxin type A  
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C39, 1G6, 3D12, B4, 1F3, hUC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)

CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surpluses. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of a linker associated with the anti-BoNT/A-antibodies of the  
 CC invention. Note: This sequence is found in the sequence listing but is  
 CC not further described in the specification.

SQ Sequence 15 AA;  
 Query Match 100.0%; Score 66; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 0.012;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSSSSSSSG 15  
 |||||  
 Db 1 SSSSGSSSSSSSSSG 15

RESULT 8  
 AA67939  
 ID AA67939 standard; peptide; 17 AA.  
 AC AA67939;  
 XX  
 DT 27-MAR-2000 (first entry)  
 XX  
 DE EPoA-hSA fusion protein peptide linker #2.  
 XX  
 KW Erythropoietin analogue human serum albumin fusion protein; infection;  
 KM EPoA-hSA fusion protein; peptide linker; HIV; cytostatic; antianemic;  
 KW anaemia; renal failure; blood loss; cancer; nutraceutical; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9966054-A2.  
 XX  
 PD 23-DEC-1999.  
 XX  
 PF 15-JUN-1999; 99WO-US013438.  
 XX  
 PR 15-JUN-1998; 98US-0089343P.  
 XX  
 PA (GENZ ) GENZYME TRANSGENICS CORP.  
 XX  
 PI Young MW, Meade HM, Krane IW;  
 PI  
 DR WPI; 2000-097749/08.  
 XX  
 PT An erythropoietin analog-human serum albumin fusion protein, used for,  
 PT e.g. treatment of HIV infection.  
 XX  
 PS Claim 19; Page 53; 61pp; English.  
 XX  
 CC The present invention describes erythropoietin analogue-human serum  
 CC albumin (EPoA-hSA) fusion proteins having at least one amino acid residue  
 CC of the EPoA moiety altered such that a site, which serves as a site for  
 CC glycosylation in EPO does not serve same purpose in the EPoA. The present  
 CC sequence represents a specifically claimed peptide linker for use in the  
 CC construction of an EPoA-hSA fusion protein. The EPoA-hSA fusion protein



CC can be used in treatment of a subject in need of EPO, e.g. for a patient  
CC suffering from anemia associated with renal failure, chronic disease  
CC HIV infection, blood loss or cancer. The EPO-hsa fusion protein can be  
CC included in a nutraceutical, such as an infant feeding formula. The EPO-  
CC hsa constructs can be used as part of a gene therapy protocol to deliver  
CC nucleic acids encoding an EPO-hsa fusion protein  
CC  
XX

8Q Sequence 17 AA;

Query Match 100.0%; Score 66; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSGSSSSG 15  
Db 1 SSSSGSSSGSSSSG 15  
|||||

RESULT 9

AA017004 standard; peptide; 17 AA.

AC AA017004;

DT 29-MAY-2002 (first entry)

DE Linker peptide used to construct alpha-MSH concatamer SEQ ID NO: 68.

XX Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis;  
KW alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma;  
KW cirrhosis; dermatitis; psoriasis; inflammatory bowel disease;  
KW immunosuppressive; antiinflammatory; antirheumatic; antiarthritic;  
KW antidiabetic; antibacterial; dermatological; antipsoriatic;  
KW antidiabetic; ophthalmological; neuroprotective; multiple sclerosis;  
KW diabetes; uveitis; coeliac disease; linker.

OS Synthetic.

PN WO200206316-A2.

PD 24-JAN-2002.

PF 16-JUL-2001; 2001WO-US022263.

PR 14-JUL-2000; 2000US-0218381P.

PR 18-AUG-2000; 2000US-0226382P.

PR 06-OCT-2000; 2000US-0238380P.

PR 29-DEC-2000; 2000US-0258764P.

PR 14-JUN-2001; 2001US-0298317P.

PA (ZYCO-) ZYCO INC.

PI Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;

DR WPI; 2002-195801/25.

XX Novel nucleic acid encoding fusion protein comprising alpha-melanocyte  
PT stimulating hormone concatamer or its analog, for treating inflammatory  
PT or autoimmune disorders.

PS Disclosure; Page 16; 89pp; English.

CC The present invention relates to a nucleic acid comprising a sequence  
CC encoding a fusion polypeptide having an alpha-melanocyte stimulating  
CC hormone (MSH) concatamer. The sequences are useful for treating an  
CC individual suffering from, or at risk of, a disorder of the immune system  
CC e.g. inflammatory disorder or autoimmune disorder, including rheumatoid  
CC arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact  
CC hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,  
CC multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The  
CC present sequence is a linker peptide described in the exemplification of  
CC the invention

8Q Sequence 17 AA;

Query Match 100.0%; Score 66; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSGSSSSG 15  
Db 1 SSSSGSSSGSSSSG 15  
|||||

RESULT 10

ADB24918 standard; peptide; 17 AA.

AC ADB24918;

DT 20-NOV-2003 (first entry)

DE Peptide linker #4.

XX antibody generation; rapid protein production;  
KW efficient protein production; linker.

OS Synthetic.

PN US2003049801-A1.

PD 13-MAR-2003.

PF 14-FEB-2002; 2002US-00077210.

PR 10-SEP-2001; 2001US-0318474P.

PA (WUCC/) WU C.

PA (LINR/) LIN R.

PA (HSUP/) HSU P.

PI Wu C, Lin R, Hsu P;

DR WPI; 2003-605754/57.

PT Generating an antibody for basic research and therapeutic purposes,  
PT comprises producing a fusion protein in a first mammal and administering  
PT the formed protein to a second mammal to generate an antibody against the  
PT protein.

PS Disclosure; Page 3; 9pp; English.

CC The invention relates to a method of generating an antibody. The method  
CC is useful in generating antibodies that may be used for basic research  
CC and in the diagnosis and treatment of various diseases. The antibodies  
CC may allow for the precise identification and quantitation of a particular  
CC species of protein in a biological sample. The antibody may also be used  
CC to modulate the activity or function of a protein which is useful for  
CC treating a disease characterised by excessive or insufficient activity of  
CC the protein. The method allows for the rapid and efficient production and  
CC isolation of large amounts of protein or its portion in its native  
CC conformation. The method avoids the time-consuming, expensive and  
CC laborious tasks associated with the in vitro production and purification  
CC of proteins. The present sequence represents a peptide linker.

8Q Sequence 17 AA;

Query Match 100.0%; Score 66; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSGSSSSG 15  
Db 1 SSSSGSSSGSSSSG 15  
|||||

RESULT 11  
ADB24915  
ID ADB24915 standard; peptide; 17 AA.  
XX  
AC ADB24915;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Peptide linker #4.  
XX  
KM fusion protein purification; rapid protein production;  
KW efficient protein production; high-throughput screening; linker.  
XX  
OS Synthetic.  
XX  
PN US2003049694-A1.  
XX  
PD 13-MAR-2003.  
XX  
PF 14-FEB-2002; 2002US-00077213.  
XX  
PR 10-SEP-2001; 2001US-0318474P.  
XX  
PA (WUCC/) WU C.  
PA (LINR/) LIN R.  
PA (HSUP/) HSU P.  
XX  
PI Wu C, Lin R, Hsu P;  
XX  
DR WPI; 2003-615799/58.  
XX  
PT Preparing purified fusion proteins useful to screen for target binding  
PT molecule, by administering nucleic acid encoding the fusion protein to a  
PT mammal, and isolating the fusion protein by removing a biological sample  
PT from mammal.  
XX  
PS Disclosure; Page 3; 9pp; English.  
XX  
CC The invention relates to a method of preparing a purified fusion protein.  
CC The method is useful for preparing fusion proteins. The method allows for  
CC rapid and efficient, production and isolation of a protein encoded by any  
CC nucleic acid sequence of interest. The method permits the high-throughput  
CC screening of antibodies or other ligands directed against any protein  
CC sequence, without the need to synthesise the protein sequence in vitro.  
CC The method avoids the time-consuming, expensive and laborious tasks  
CC associated with the in vitro production and purification of proteins. The  
CC method avoids several of the difficulties associated with recombination  
CC protein production in bacteria. The present sequence represents a peptide  
CC linker.  
XX  
SQ Sequence 17 AA;  
XX  
Query Match 100.0%; Score 66; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSSSSSSSSSSSSSG 15  
Db 1 SSSSSSSSSSSSSSG 15  
XX  
RESULT 12  
ABU10017  
ID ABU10017 standard; peptide; 17 AA.  
XX  
AC ABU10017;  
XX  
DT 31-JUL-2003 (first entry)  
XX  
DE Alpha-MSH concatamer related linker peptide #5.  
XX  
KM Bladder disorder; cytostatic; antiinflammatory; immune response;  
KW un-methylated CpG sequence; alpha-MSH; melanocortin receptor;  
XX

KW bladder cancer; tumour; interstitial cystitis; inflammation; alpha-MSH;  
KW melanocyte stimulating hormone.  
XX  
OS Unidentified.  
XX  
PN US2002193332-A1.  
XX  
PD 19-DEC-2002.  
XX  
PF 12-FEB-2002; 2002US-00074956.  
XX  
PR 12-FEB-2001; 2001US-0268175P.  
XX  
PA (HEDL/) HEDLEY M L.  
XX  
PI Hedley ML;  
XX  
DR WPI; 2003-447327/42.  
XX  
PT Modulating immune responses in a mammal with a bladder disorder e.g.  
PT bladder cancer, by administering nucleic acids comprising un-methylated  
PT CpG sequences, nucleic acids encoding alpha-MSH, or alpha-MSH peptides to  
PT the mammal.  
XX  
PS Disclosure; Page 5; 17pp; English.  
XX  
CC The invention describes a method of modulating an immune response in a  
CC mammal, comprising identifying a mammal that has or is at risk for having  
CC a bladder disorder, and administering: (a) an isolated nucleic acid (N1)  
CC comprising an un-methylated CpG sequence to the mammal; (b) an isolated  
CC nucleic acid (N2) comprising sequence encoding alpha-MSH to the mammal;  
CC or (c) a peptide that binds to a melanocortin receptor to the mammal. The  
CC method is useful for modulating immune response in a mammal having a  
CC bladder disorder, where administration of (N1) results in an amelioration  
CC of one or more symptoms of the disorder. Preferably, the method is useful  
CC for modulating immune response in a mammal having bladder cancer (where  
CC administration of (N1) results in a decrease in tumour size or activity),  
CC or for modulating immune response in a mammal having interstitial  
CC cystitis (where administration of (N1) results in a modulation of the  
CC immune response from Th2 response to a Th1 response). The method is also  
CC useful for modulating immune response in a mammal having bladder disorder  
CC that is characterised by inflammation which is associated with symptoms  
CC of interstitial cystitis or associated with a disruption of the integrity  
CC of the bladder lining. This is the amino acid sequence of a linker  
CC peptide useful in the creation of melanocyte stimulating hormone (alpha-  
CC MSH) concatamers used in the method of treating bladder disorders  
XX  
SQ Sequence 17 AA;  
XX  
Query Match 100.0%; Score 66; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSSSSSSSSSSSSSG 15  
Db 1 SSSSSSSSSSSSSSG 15  
XX  
RESULT 13  
ADQ28276  
ID ADQ28276 standard; peptide; 17 AA.  
XX  
AC ADQ28276;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Peptide linker #4.  
XX  
KM gene therapy; transgenic; fusion protein; colon cancer; breast cancer;  
KW prostate cancer; ovarian cancer; endometrial cancer.  
XX  
OS Synthetic.  
XX

PN US2004117863-A1.  
 XX  
 PD 17-JUN-2004.  
 XX  
 XX  
 PF 27-JUN-2003; 2003US-00608710.  
 XX  
 PR 18-SEP-1998; 98US-0101083P.  
 PR 17-SEP-1999; 99US-00398610.  
 XX  
 PA (EDGE/) EDGE M D.  
 PA (POL/) POLLOCK D.  
 PA (ECHE/) ECHELARD Y.  
 PA (MEAD/) MEADE H M.  
 PA (RYBA/) RYBAK S M.  
 XX  
 PI Edge MD, Pollock D, Echelard Y, Meade HM, Rybak SM;  
 DR WPI; 2004-449486/42.  
 XX  
 PT Making a transgenic fusion protein using a transgenic animal having a  
 PT transgene expressing the fusion protein, useful for the diagnosing,  
 PT preventing or treating colon, breast, prostate, ovarian and endometrial  
 PT cancers.  
 XX  
 PS Disclosure; SEQ ID NO 9; 32pp; English.  
 XX  
 CC The invention relates to a method of making a transgenic fusion protein  
 CC comprising providing a transgenic animal which includes a transgene which  
 CC provides for the expression of the fusion protein, allowing the transgene  
 CC to be expressed, and recovering the fusion protein, from the milk of the  
 CC transgenic animal. The methods and compositions of the present invention  
 CC are useful for the diagnosis, prevention and/or treatment of colon,  
 CC breast, prostate, ovarian and endometrial cancers. The present sequence  
 CC represents the amino acid sequence of a peptide linker.  
 XX  
 SQ Sequence 17 AA:  
 Query Match 100.0%; Score 66; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 SSSSGSSSSSSSSSG 15  
 Db 1 SSSSGSSSSSSSSSG 15  
 RESULT 14  
 AAB15670  
 ID AAB15670 standard; peptide; 31 AA.  
 XX  
 AC AAB15670;  
 XX  
 DT 01-DEC-2000 (first entry)  
 XX  
 DE Alpha V beta 3 receptor-specific peptide.  
 XX  
 KW Alpha V beta 3 receptor; colloid-electrode binding; drug screening;  
 KW colloid derivatization.  
 XX  
 OS Unidentified.  
 OS  
 PN WO200043783-A2.  
 XX  
 PD 27-JUL-2000.  
 XX  
 PF 21-JAN-2000; 2000WO-US001504.  
 XX  
 PR 23-JAN-1999; 99US-0116975P.  
 PR 03-MAY-1999; 99US-0132289P.  
 PR 07-MAY-1999; 99US-0133148P.  
 PR 12-MAY-1999; 99US-0133772P.  
 XX  
 PT (MINE-) MINERVA BIOTECHNOLOGIES CORP.  
 PA

XX  
 PI Bamdad CC, Bamdad RS;  
 XX  
 DR WPI; 2000-514740/46.  
 XX  
 PT Interaction of colloid-immobilized species with species on non-colloidal  
 PT structures, useful in assays for monitoring or detecting interactions  
 PT between chemical or biological species, particularly for drug screening.  
 XX  
 PS Example 43; Page 35; 95pp; English.  
 XX  
 CC The present sequence is a peptide which was used in an example describing  
 CC the electronic detection of cells grown on conducting surfaces that were  
 CC not coated with collagen. Cells were incubated with colloids that  
 CC displayed ferrocene moieties and the present peptide, which is specific  
 CC for the alpha V beta 3 receptor on the cell surface. Cells grown on a  
 CC 100% ethynylphenyl thiol SAM-coated electrode produced current peaks only  
 CC if incubated with colloids bearing the ligand specific for the alpha V  
 CC beta 3 receptor and not when incubated with colloids derivatised with an  
 CC irrelevant peptide. This example was used to demonstrate a method for  
 CC enabling colloids to bind to non-colloidal structures such as electrodes,  
 CC beads or cells. The method is useful in assays for monitoring or  
 CC detecting interactions between chemical or biological species,  
 CC particularly for drug screening, screening for inhibitors or activators  
 CC of enzymes, identifying unknown targets or known ligands, detection of  
 CC protein-protein interactions, detection of protein-ligand interactions,  
 CC and detection of ligand-receptor interactions  
 XX  
 SQ Sequence 31 AA:  
 Query Match 100.0%; Score 66; DB 3; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 0.026;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 SSSSGSSSSSSSSSG 15  
 Db 7 SSSSGSSSSSSSSSG 21  
 RESULT 15  
 AA022543  
 ID AA022543 standard; peptide; 31 AA.  
 XX  
 AC AA022543;  
 XX  
 DT 28-OCT-2002 (first entry)  
 XX  
 DE GRGDS-containing peptide.  
 XX  
 KW Cytostatic; antitumour; angiogenesis inhibitor; L-histidine; suramin;  
 KW quiescent acid; D-cycloserine; invasive cancer; metastatic tumour;  
 KW endostatin; nanoparticle-based; alpha-V-beta3-vitronectin interaction;  
 KW vitronectin.  
 XX  
 OS Unidentified.  
 OS  
 PN WO200239999-A2.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 15-NOV-2001; 2001WO-US046221.  
 XX  
 PR 15-NOV-2000; 2000US-024865P.  
 PR 22-MAR-2001; 2001US-0279222P.  
 XX  
 PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.  
 XX  
 PI Bamdad RS, Bamdad CC;  
 XX  
 DR WPI; 2002-490116/52.  
 XX  
 PT Use of a composition comprising L-histidine, quiescent acid, D-  
 PT cycloserine, and suramin or their analogs for the treatment of invasive

PT cancer and metastatic tumors.

XX  
PS Example 2; Page 4; 27pp; English.

XX  
CC The invention relates to the treatment of a human patient involving the  
CC administering of a composition comprising an angiogenesis inhibitor  
CC selected from L-histidine, quisqualic acid, D-cycloserine or suramin or  
CC their analogues to the patient. The treatment is useful against invasive  
CC cancer and metastatic tumours. The advantage of the treatment is that the  
CC composition can be given at a maximum amount while avoiding detrimental  
CC side effects. The method provides a molecular target of the known  
CC angiogenesis inhibitor, endostatin, and provides a high throughput,  
CC nanoparticle-based in vitro assay that rapidly identifies compounds, both  
CC natural and synthetic that inhibit angiogenesis by mimicking the effect  
CC of endostatin. The compounds are readily modified and optimised to  
CC produce analogues that are more effective than the parent compound. This  
CC sequence represents a GRGDS-containing peptide of the invention. The  
CC GRGDS peptide mimics full-length vitronectin and inhibits angiogenesis by  
CC interrupting the alpha-V-beta3-vitronectin interaction relating to the  
CC invention

XX  
SQ Sequence 31 AA;

Query Match 100.0%; Score 66; DB 5; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.026;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSSG 15

DB 7 SSSSSSSSSSSSSSSG 21

Search completed: April 4, 2005, 15:47:21  
Job time : 30.9521 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 7.66773 Seconds

(without alignments)  
146.032 Million cell updates/sec

Title: US-09-887-853-8

Perfect score: 66

Sequence: 1 SSSSSSSSSSSSSSSG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A COMB pep:\*

2: /cgn2\_6/ptodata/1/1aa/5B COMB pep:\*

3: /cgn2\_6/ptodata/1/1aa/6A COMB pep:\*

4: /cgn2\_6/ptodata/1/1aa/6B COMB pep:\*

5: /cgn2\_6/ptodata/1/1aa/6CTUS COMB pep:\*

6: /cgn2\_6/ptodata/1/1aa/backfile1.pdp:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	15	1	US-08-133-804-8
2	66	100.0	15	1	US-08-461-838-8
3	66	100.0	15	2	US-08-461-386-8
4	66	100.0	15	2	US-08-356-786-12
5	66	100.0	15	2	US-08-665-202-3
6	66	100.0	15	3	US-08-483-749A-31
7	66	100.0	15	4	US-09-315-574-3
8	66	100.0	15	4	US-09-324-258-18
9	66	100.0	17	4	US-09-333-213-4
10	66	100.0	17	4	US-10-077-210-4
11	66	100.0	31	4	US-09-324-258-19
12	66	100.0	100	4	US-09-411-067C-5
13	66	100.0	243	1	US-08-133-804-6
14	66	100.0	243	1	US-08-461-838-6
15	66	100.0	243	2	US-08-461-386-6
16	66	100.0	243	2	US-08-356-786-4
17	62	93.9	246	1	US-08-257-341-7
18	62	93.9	252	1	US-08-133-804-4
19	62	93.9	252	2	US-08-461-838-4
20	62	93.9	252	2	US-08-461-386-4
21	62	93.9	367	1	US-08-257-341-5
22	62	93.9	471	1	US-08-257-341-9
23	60	90.9	250	1	US-08-133-804-2
24	60	90.9	250	1	US-08-461-184-8
25	60	90.9	250	1	US-08-463-675-8
26	60	90.9	250	1	US-08-464-589-8
27	60	90.9	250	1	US-08-461-838-2

28	60	90.9	250	2	US-08-461-386-2	Sequence 2, Appl1
29	60	90.9	622	2	US-08-356-786-16	Sequence 16, Appl1
30	57	86.4	212	4	US-09-270-767-41907	Sequence 41907, A
31	54	81.8	13	1	US-08-257-341-1	Sequence 1, Appl1
32	54	81.8	239	4	US-09-248-796A-16550	Sequence 16550, A
33	54	81.8	408	4	US-09-543-681A-6442	Sequence 6442, Ap
34	54	81.8	475	2	US-08-861-464-14	Sequence 14, Appl1
35	54	81.8	475	2	US-08-396-001-14	Sequence 14, Appl1
36	54	81.8	475	3	US-09-323-433A-14	Sequence 14, Appl1
37	54	81.8	475	4	US-09-826-752-14	Sequence 14, Appl1
38	54	81.8	1481	2	US-08-616-844-40	Sequence 40, Appl1
39	54	81.8	1481	2	US-08-599-654-40	Sequence 40, Appl1
40	54	81.8	1481	3	US-08-944-868A-40	Sequence 40, Appl1
41	54	81.8	1481	3	US-08-944-423A-40	Sequence 40, Appl1
42	54	81.8	1481	3	US-08-944-436-40	Sequence 40, Appl1
43	53	80.3	180	4	US-09-248-796A-22352	Sequence 22352, A
44	53	80.3	250	4	US-09-248-796A-22487	Sequence 22487, A
45	53	80.3	442	4	US-09-248-796A-21400	Sequence 21400, A

#### ALIGNMENTS

RESULT 1  
US-08-133-804-8  
Sequence 8, Application US/08133804  
Patent No. 5534254  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppertmann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
NUMBER OF SEQUENCES: 11  
TITLE OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/133.804  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURES:  
NAME/KEY: Protein  
LOCATION: 1..15  
OTHER INFORMATION: /note= "LINKER 2"  
US-08-133-804-8  
Query Match 100.0%; Score 66; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0087;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSG 15

Db 1 SSSSSSSSSSSSSG 15

## RESULT 2

US-08-461-838-8

; Sequence 8, Application US/08461838

; Patent No. 5753204

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Oppermann, Hermann

; APPLICANT: Houston, L. L.

; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; TELEFAX: 617-248-7100

; TELEPHONE: 617-248-7477

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..15

; OTHER INFORMATION: /note= "LINKER 2"

US-08-461-838-8

Query Match 100.0%; Score 66; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.0087;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSG 15

Db 1 SSSSSSSSSSSSSG 15

## RESULT 3

US-08-461-386-8

; Sequence 8, Application US/08461386

; Patent No. 5837846

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Oppermann, Hermann

; APPLICANT: Houston, L. L.

; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; TELEFAX: 617-248-7100

; TELEPHONE: 617-248-7477

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..15

; OTHER INFORMATION: /note= "LINKER 2"

US-08-461-386-8

Query Match 100.0%; Score 66; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.0087;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSG 15

Db 1 SSSSSSSSSSSSSG 15

; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; TELEFAX: 617-248-7100

; TELEPHONE: 617-248-7477

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..15

; OTHER INFORMATION: /note= "LINKER 2"

US-08-461-386-8

Query Match 100.0%; Score 66; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.0087;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSG 15

Db 1 SSSSSSSSSSSSSG 15

## RESULT 4

US-08-356-786-12

; Sequence 12, Application US/08356786

; Patent No. 5877305

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Oppermann, Hermann

; APPLICANT: Houston, L. L.

; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; TELEFAX: 617-248-7100

; TELEPHONE: 617-248-7477

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..15

; OTHER INFORMATION: /note= "LINKER 2"

US-08-461-386-8

Query Match 100.0%; Score 66; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.0087;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSG 15

Db 1 SSSSSSSSSSSSSG 15

APPLICATION NUMBER: US/08/356,786  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/831,967  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-786-12

Query Match 100.0%; Score 66; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0087;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSSSSSSSG 15  
DB 1 SSSSGSSSSSSSSSG 15

RESULT 5  
US-08-665-202-3  
Sequence 3, Application US/08665202  
Patent No. 5977322  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.  
APPLICANT: Schier, Robert  
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,202  
FILING DATE: 13-JUN-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061410  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-665-202-3

Query Match 100.0%; Score 66; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0087;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSSSSSSSG 15  
DB 1 SSSSGSSSSSSSSSG 15

RESULT 6  
US-08-483-749A-31  
Sequence 31, Application US/08483749A  
Patent No. 6054561  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
CITY: EMERYVILLE  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,749A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVERIDE, PAUL B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0508,008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-483-749A-31

Query Match 100.0%; Score 66; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0087;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSSSSSSSG 15  
DB 1 SSSSGSSSSSSSSSG 15

RESULT 7  
US-09-315-574-3  
Sequence 3, Application US/09315574  
Patent No. 6512097  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.  
APPLICANT: Schier, Robert  
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to  
NUMBER OF SEQUENCES: 141

```

CORRESPONDENCE ADDRESS:
ADDRESS: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-3

Query Match      100.0%; Score 66; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSSSGSSSGSSSGSSG 15
DB      1 SSSSGSSSGSSSGSSG 15

RESULT 8
US-09-324-258-18
Sequence 18, Application US/09324258
Patent No. 6723517
GENERAL INFORMATION:
APPLICANT: Bamdad, Cynthia C.
TITLE OF INVENTION: THE USE OF SELF-ASSEMBLED MONOLAYERS TO
FILE REFERENCE: M1015/7004/TJO
CURRENT APPLICATION NUMBER: US/09/324,258
CURRENT FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: U.S. 60/087,766
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: linker
US-09-324-258-18
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Query Match      100.0%; Score 66; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSSSGSSSGSSSGSSG 15
DB      1 SSSSGSSSGSSSGSSG 15

RESULT 9
US-09-333-213-4
Sequence 4, Application US/09333213
Patent No. 6548653
GENERAL INFORMATION:
APPLICANT: Young, Michael
APPLICANT: Meade, Harry
APPLICANT: Krane, Ian
TITLE OF INVENTION: ERYTHROPOIETIN ANALOGY-HUMAN SERUM ALBUMIN FUSION
FILE REFERENCE: 10275/041001
CURRENT APPLICATION NUMBER: US/09/333,213
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated linker sequence
US-09-333-213-4

Query Match      100.0%; Score 66; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSSSGSSSGSSSGSSG 15
DB      1 SSSSGSSSGSSSGSSG 15

RESULT 10
US-10-077-210-4
Sequence 4, Application US/10077210
Patent No. 6800462
GENERAL INFORMATION:
APPLICANT: Wu, Chung-Hsiun
APPLICANT: Lin, Rong-Hwa
APPLICANT: Hsu, Pei-Ling
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT PROTEINS IN VIVO AND USE FOR GENERATING
FILE REFERENCE: 13062-004001
CURRENT APPLICATION NUMBER: US/10/077,210
CURRENT FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: 60/318,474
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Linker sequence
US-10-077-210-4

Query Match      100.0%; Score 66; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSSSGSSSGSSSGSSG 15
DB      1 SSSSGSSSGSSSGSSG 15
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RESULT 11
US-09-324-258-19
; Sequence 19, Application US/09324258
; Patent No. 6723517
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia C.
; TITLE OF INVENTION: THE USE OF SELF-ASSEMBLED MONOLAYERS TO
; FILE REFERENCE: M1015/7004/TUO
; CURRENT FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: U.S. 60/087,766
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IX-Linker-1X
US-09-324-258-19

Query Match          100.0%; Score 66; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSSGSSSSSSSSSG 15
Db 9 SSSSGSSSSSSSSSG 23

RESULT 12
US-09-411-067C-5
; Sequence 5, Application US/09411067C
; Patent No. 6576610
; GENERAL INFORMATION:
; APPLICANT: NUVAS, LLC
; APPLICANT: HOUSTON, L.L.
; TITLE OF INVENTION: USE OF A CONTEXT-DEPENDENT FUNCTIONAL ENTITY TO ENHANCE THE EFFIC
; FILE REFERENCE: NUVAS1140
; CURRENT APPLICATION NUMBER: US/09/411,067C
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Spacer element
; NAME/KEY: REPEAT
; LOCATION: (1)..(5)
; OTHER INFORMATION: Spacer peptide variation; sequence repeated "n" times, where n =
US-09-411-067C-5

Query Match          100.0%; Score 66; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSSGSSSSSSSSSG 15
Db 1 SSSSGSSSSSSSSSG 15

RESULT 13
US-08-133-804-6
; Sequence 6, Application US/08133804
; Patent No. 5534254
```

```
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Testa, Hurwitz & Thibault/Parent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/133,804
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-133-804-6

Query Match          100.0%; Score 66; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSSGSSSSSSSSSG 15
Db 118 SSSSGSSSSSSSSSG 132

RESULT 14
US-08-461-838-6
; Sequence 6, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Testa, Hurwitz & Thibault/Parent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/461,838  
FILING DATE: 424  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-461-838-6

Query Match 100.0%; Score 66; DB 1; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSGSSSG 15  
|||  
Db 118 SSSSGSSSGSSSG 132

RESULT 15  
US-08-461-386-6  
Sequence 6, Application US/08461386  
Patent No. 5837846

GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
TITLE OF INVENTION: Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,386  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-461-386-6

Query Match 100.0%; Score 66; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSGSSSG 15  
|||  
Db 118 SSSSGSSSGSSSG 132

Search completed: April 4, 2005, 16:00:54  
Job time : 8.66773 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 22.1406 Seconds  
(without alignments)  
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Title: US-09-887-853-8  
Perfect score: 66  
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Scoring table: BLOSUM62  
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Searched: 1413372 seqs, 331592847 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 4: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	15	9	US-09-144-886-3
2	66	100.0	15	9	US-09-887-853-8
3	66	100.0	15	15	US-10-204-581-1
4	66	100.0	15	15	US-10-632-706-3
5	66	100.0	15	17	US-10-683-547-8
6	66	100.0	17	13	US-10-081-400-4
7	66	100.0	17	13	US-10-074-956-19
8	66	100.0	17	14	US-10-077-213-4
9	66	100.0	17	14	US-10-077-210-4
10	66	100.0	17	16	US-10-608-710-9
11	66	100.0	17	16	US-10-768-873-4
12	66	100.0	31	10	US-09-996-069-12
13	66	100.0	31	13	US-10-003-661-1

14	66	100.0	243	9	US-09-887-853-6	Sequence 6, Appl1
15	66	100.0	252	17	US-10-683-547-6	Sequence 6, Appl1
16	62	93.9	252	17	US-09-887-853-4	Sequence 4, Appl1
17	62	93.9	252	17	US-10-683-547-4	Sequence 4, Appl1
18	60	90.9	250	9	US-09-887-853-2	Sequence 2, Appl1
19	60	90.9	250	17	US-10-683-547-2	Sequence 2, Appl1
20	57	86.4	1249	15	US-10-369-493-6099	Sequence 6099, Ap
21	56	84.8	123	15	US-10-767-701-35941	Sequence 35941, A
22	55	83.3	563	16	US-10-437-963-198539	Sequence 198539,
23	54	81.8	94	9	US-09-764-864-1273	Sequence 1273, Ap
24	54	81.8	104	9	US-09-764-864-1276	Sequence 1276, Ap
25	54	81.8	108	9	US-09-764-864-817	Sequence 817, Ap
26	54	81.8	112	9	US-09-764-864-812	Sequence 812, Ap
27	54	81.8	156	9	US-09-925-301-1154	Sequence 1154, Ap
28	54	81.8	160	15	US-10-424-5599-175646	Sequence 175646,
29	54	81.8	179	16	US-10-437-963-199226	Sequence 199226,
30	54	81.8	203	15	US-10-264-237-1938	Sequence 1938, Ap
31	54	81.8	256	14	US-10-156-761-11972	Sequence 11972, A
32	54	81.8	386	14	US-10-050-704-100	Sequence 100, App
33	54	81.8	386	16	US-10-798-512-100	Sequence 100, App
34	54	81.8	406	16	US-10-451-467A-262	Sequence 262, App
35	54	81.8	448	15	US-10-108-260A-2481	Sequence 2481, Ap
36	54	81.8	472	15	US-10-258-951-73	Sequence 73, Appl
37	54	81.8	475	9	US-09-826-752-14	Sequence 14, Appl
38	54	81.8	475	15	US-10-369-493-32092	Sequence 22092, A
39	54	81.8	475	17	US-10-912-434-14	Sequence 14, Appl
40	54	81.8	544	14	US-10-032-585-7924	Sequence 7924, Ap
41	54	81.8	593	15	US-10-258-951-72	Sequence 72, Appl
42	54	81.8	623	13	US-10-108-605-125	Sequence 125, App
43	54	81.8	623	13	US-10-108-605-129	Sequence 129, App
44	54	81.8	679	15	US-10-282-122A-78228	Sequence 78228, A
45	54	81.8	946	10	US-09-840-746-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-09-144-886-3  
; Sequence 3, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; FILE REFERENCE: 2500.117USO  
; CURRENT APPLICATION NUMBER: US/09/144, 886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: [(Ser)4Gly]3  
; OTHER INFORMATION: Linker  
US-09-144-886-3

Query Match 100.0%; Score 66; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.062;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSG 15  
DB 1 SSSSSSSSSSSSSSG 15

RESULT 2  
US-09-887-853-8  
; Sequence 8, Application US/09887853  
; Patent No. US20020168375A1

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; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
;               Oppermann, Hermann
;               Houston, L. L.
;               Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
;                   Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/887,853
; FILING DATE: 21-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..15
; OTHER INFORMATION: /note="LINKER 2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
; US-09-887-853-8
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; Query Match      100.0%; Score 66; DB 9; Length 15;
; Best Local Similarity 100.0%; Pred. No. 0.062;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY      1 SSSSGSSSSSSSSSG 15
;         |||||
; Db      1 SSSSGSSSSSSSSSG 15
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; RESULT 3
; US-10-204-581-1
; Sequence 1, Application US/10204581
; Publication No. US20040013640A1
; GENERAL INFORMATION:
; APPLICANT: Zardi, Luciano
; APPLICANT: Neri, Dario
; APPLICANT: Carmemolla, Barbara
; APPLICANT: Nilsson, Fredrik
; APPLICANT: Tarli, Lorenzo
; APPLICANT: Borsi, Laura
; APPLICANT: Halin, Cornelia
; TITLE OF INVENTION: Compositions and methods for treatment of angiogenesis
; FILE REFERENCE: 0380-P02964US0
; CURRENT APPLICATION NUMBER: US/10/204,581

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; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/IB01/00382
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/184,767
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/257,192
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Linker
; US-10-204-581-1
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; Query Match      100.0%; Score 66; DB 15; Length 15;
; Best Local Similarity 100.0%; Pred. No. 0.062;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY      1 SSSSGSSSSSSSSSG 15
;         |||||
; Db      1 SSSSGSSSSSSSSSG 15
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; RESULT 4
; US-10-632-706-3
; Sequence 3, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: protein linker
; US-10-632-706-3
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; Query Match      100.0%; Score 66; DB 16; Length 15;
; Best Local Similarity 100.0%; Pred. No. 0.062;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY      1 SSSSGSSSSSSSSSG 15
;         |||||
; Db      1 SSSSGSSSSSSSSSG 15
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; RESULT 5
; US-10-683-547-8
; Sequence 8, Application US/10683547
; Publication No. US20050058638A1
; GENERAL INFORMATION:
; APPLICANT: Huston, J.
; APPLICANT: Houston, L.L.
; APPLICANT: Ring, D.
; APPLICANT: Oppermann, H.
; TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
; FILE REFERENCE: CIBT-P01-130
; CURRENT APPLICATION NUMBER: US/10/683,547

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/ CURRENT FILING DATE: 2003-10-10
/ PRIOR APPLICATION NUMBER: US/09/558,741
/ PRIOR FILING DATE: 2000-04-26
/ PRIOR APPLICATION NUMBER: 07/831,967
/ PRIOR FILING DATE: 1992-02-06
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 8
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Linker 2
US-10-683-547-8
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Query Match      100.0%; Score 66; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 SSSSSSSSSSSSSSG 15
Db      1 SSSSSSSSSSSSSSG 15
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RESULT 6
US-10-081-400-4
/ Sequence 4, Application US/10081400
/ Publication No. US2002015598A1
/ GENERAL INFORMATION:
/ APPLICANT: Young, Michael
/ APPLICANT: Meade, Harry
/ APPLICANT: Krane, Ian
/ TITLE OF INVENTION: ERYTHROPOIETIN ANALOGY-HUMAN SERUM ALBUMIN FUSION
/ FILE REFERENCE: 10215/041001
/ CURRENT APPLICATION NUMBER: US/10/081,400
/ CURRENT FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 09/333,213
/ PRIOR FILING DATE: 1999-06-15
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetically generated linker sequence
US-10-081-400-4
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Query Match      100.0%; Score 66; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 SSSSSSSSSSSSSSG 15
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RESULT 7
US-10-074-956-19
/ Sequence 19, Application US/10074956
/ Publication No. US20020193332A1
/ GENERAL INFORMATION:
/ APPLICANT: Hedley, Mary Lynne
/ TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
/ FILE REFERENCE: 08191-022001
/ CURRENT APPLICATION NUMBER: US/10/074,956
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: 60/268,175
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 19
/ LENGTH: 17
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/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-074-956-19
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Query Match      100.0%; Score 66; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 SSSSSSSSSSSSSSG 15
Db      1 SSSSSSSSSSSSSSG 15
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RESULT 8
US-10-077-213-4
/ Sequence 4, Application US/10077213
/ Publication No. US20030049694A1
/ GENERAL INFORMATION:
/ APPLICANT: Wu, Chung-Hsiun
/ APPLICANT: Lin, Rong-Hwa
/ APPLICANT: Hsu, Pei-Ling
/ TITLE OF INVENTION: PRODUCTION OF FUSION PROTEINS AND USE
/ FILE REFERENCE: 13062-002001
/ CURRENT APPLICATION NUMBER: US/10/077,213
/ CURRENT FILING DATE: 2002-06-13
/ PRIOR APPLICATION NUMBER: 60/318,474
/ PRIOR FILING DATE: 2001-09-10
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Linker sequence
US-10-077-213-4
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Query Match      100.0%; Score 66; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 SSSSSSSSSSSSSSG 15
Db      1 SSSSSSSSSSSSSSG 15
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RESULT 9
US-10-077-210-4
/ Sequence 4, Application US/10077210
/ Publication No. US20030049801A1
/ GENERAL INFORMATION:
/ APPLICANT: Wu, Chung-Hsiun
/ APPLICANT: Lin, Rong-Hwa
/ APPLICANT: Hsu, Pei-Ling
/ TITLE OF INVENTION: PRODUCTION OF RECOMBINANT PROTEINS IN VIVO AND USE FOR GENERATING
/ FILE REFERENCE: 13062-004001
/ CURRENT APPLICATION NUMBER: US/10/077,210
/ CURRENT FILING DATE: 2002-06-13
/ PRIOR APPLICATION NUMBER: 60/318,474
/ PRIOR FILING DATE: 2001-09-10
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Linker sequence
US-10-077-210-4

Query Match      100.0%; Score 66; DB 14; Length 17;
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Best Local Similarity 100.0%; Pred. No. 0.069;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 SSSSSSSSSSSSSSG 15

RESULT 10  
US-10-608-710-9  
; Sequence 9, Application US/10608710  
; Publication No. US20040117863A1  
; GENERAL INFORMATION:  
; APPLICANT: GTC Biopharmaceutics, Inc.  
; APPLICANT: Edge, Michael D  
; APPLICANT: Pollock, Daniel  
; APPLICANT: Echeleard, Yann  
; APPLICANT: Meade, Harry M  
; APPLICANT: Rybak, Susana M  
; TITLE OF INVENTION: Transgenically Produced Fusion Proteins  
; FILE REFERENCE: GTC-42D  
; CURRENT APPLICATION NUMBER: US/10/608,710  
; CURRENT FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: US 09/398,610  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: peptide linker  
US-10-608-710-9

Query Match 100.0%; Score 66; DB 16; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.069;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSG 15  
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Db 1 SSSSSSSSSSSSSSG 15

RESULT 11  
US-10-768-873-4  
; Sequence 4, Application US/10768873  
; Publication No. US20040143857A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Michael  
; APPLICANT: Meade, Harry  
; APPLICANT: Krane, Ian  
; TITLE OF INVENTION: ERYTHROPOIETIN ANALOGY-HUMAN SERUM ALBUMIN FUSION  
; FILE REFERENCE: 10275/041001  
; CURRENT APPLICATION NUMBER: US/10/768,873  
; CURRENT FILING DATE: 2004-01-30  
; PRIOR APPLICATION NUMBER: US/09/333,213  
; PRIOR FILING DATE: 1999-06-15  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated linker sequence  
US-10-768-873-4

Query Match 100.0%; Score 66; DB 16; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.069;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSG 15  
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Db 1 SSSSSSSSSSSSSSG 15

RESULT 12  
US-09-996-069-12

; Sequence 12, Application US/09996069  
; Publication No. US20030036199A1  
; GENERAL INFORMATION:  
; APPLICANT: Bamdad, Cynthia  
; APPLICANT: Bamdad, R. Shoshana  
; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBIT  
; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER  
; FILE REFERENCE: M01015/70071  
; CURRENT APPLICATION NUMBER: US/09/996,069  
; CURRENT FILING DATE: 2001-11-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-069-12

Query Match 100.0%; Score 66; DB 10; Length 31;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSG 15  
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Db 7 SSSSSSSSSSSSSSG 21

RESULT 13  
US-10-003-681-1  
; Sequence 1, Application US/10003681  
; Publication No. US20020156112A1  
; GENERAL INFORMATION:  
; APPLICANT: Bamdad, R. Shoshana  
; APPLICANT: Bamdad, Cynthia  
; TITLE OF INVENTION: ENDOSTATIN-LIKE ANGIOGENESIS INHIBITION  
; FILE REFERENCE: M01015-70046-US  
; CURRENT APPLICATION NUMBER: US/10/003,681  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/248,865  
; PRIOR FILING DATE: 2000-11-15  
; PRIOR APPLICATION NUMBER: US 60/277,922  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic sequence  
US-10-003-681-1

Query Match 100.0%; Score 66; DB 13; Length 31;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSG 15  
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Db 7 SSSSSSSSSSSSSSG 21

RESULT 14  
US-09-887-853-6  
; Sequence 6, Application US/09887853  
; Patent No. US20020168375A1  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.

Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Teesta, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/887,853  
FILING DATE: 21-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/133,804  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-887-853-6

Query Match 100.0%; Score 66; DB 9; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.86;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSGSSSG 15  
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Db 118 SSSSGSSSGSSSG 132

RESULT 15  
US-10-683-547-6  
Sequence 6, Application US/10683547  
Publication No. US20050058638A1  
GENERAL INFORMATION:  
APPLICANT: Houston, J.  
APPLICANT: Houston, L.L.  
APPLICANT: Ring, D.  
APPLICANT: Oppermann, H.  
TITLE OF INVENTION: BIOSYNTETIC BINDING PROTEINS FOR IMMUNO-TARGETING  
FILE REFERENCE: CIBT-P01-130  
CURRENT APPLICATION NUMBER: US/10/683,547  
CURRENT FILING DATE: 2003-10-10  
PRIOR APPLICATION NUMBER: US/09/558,741  
PRIOR FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: 07/831,967  
PRIOR FILING DATE: 1992-02-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 520C9 gfv

US-10-683-547-6

Query Match 100.0%; Score 66; DB 17; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.86;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSGSSSG 15  
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Db 118 SSSSGSSSGSSSG 132

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OM protein - protein search, using sw model

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Title: US-09-887-853-8

Perfect score: 66

Sequence: 1 SSSSSSSSSSSSSSG 15

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Total number of hits satisfying chosen parameters: 283416

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

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#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	90.9	304	2	T16535
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3	57	86.4	1751	2	A45604
4	56	84.8	683	2	A82704
5	54	81.8	107	2	B85356
6	54	81.8	162	2	C85356
7	54	81.8	406	2	S38170
8	54	81.8	424	2	T08093
9	54	81.8	475	2	S49886
10	54	81.8	623	1	S33167
11	54	81.8	679	2	AC0333
12	54	81.8	1215	2	I52882
13	54	81.8	1791	2	T02345
14	54	81.8	1912	2	T29088
15	52	78.8	284	2	A35419
16	52	78.8	419	2	D83465
17	51	77.3	153	2	S67294
18	51	77.3	270	2	F86177
19	51	77.3	286	2	C61615
20	51	77.3	299	2	T12483
21	51	77.3	447	2	E83465
22	51	77.3	456	2	S69070
23	51	77.3	562	2	B41035
24	51	77.3	562	2	S50371
25	51	77.3	750	2	S04980
26	51	77.3	825	1	EDBEXD
27	51	77.3	1677	2	T43021
28	50	75.8	218	2	JC7220
29	50	75.8	335	2	T14449

30	50	75.8	380	2	T14447	oleosin homolog pc
31	50	75.8	419	2	T14448	oleosin homolog pc
32	50	75.8	440	2	S37303	box-4 protein - mo
33	50	75.8	559	1	RWBYS1	glycophospholipid-
34	50	75.8	625	2	T41603	alpha-amylose - fl
35	50	75.8	710	2	S28014	outd protein - Erw
36	50	75.8	712	2	B47021	pectic enzyme secr
37	50	75.8	741	2	I48694	probable transcrip
38	50	75.8	742	2	A49672	transcription fact
39	50	75.8	772	2	A55004	transcription fact
40	50	75.8	1029	2	T30351	mucin-like protein
41	50	75.8	1446	1	A45344	immediate-early pr
42	50	75.8	1460	1	EDBEIF	immediate-early pr
43	50	75.8	1723	2	H86557	polymorphic membra
44	50	75.8	1723	2	E72067	polymorphic membra
45	50	75.8	1732	2	C81601	polymorphic membra

#### ALIGNMENTS

##### RESULT 1

T16535

hypothetical protein K02F3.11 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C/Accession: T16535

R/Bentley, D.

submitted to the EMBL Data Library, May 1994

A/Description: The sequence of C. elegans cosmid K02F3.

A/Reference number: Z18530

A/Accession: T16535

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-304 <BEN>

A/Cross-references: EMBL:U00052; NID:9485125; PID:9485126; PIDN:AAA50702.1; CESP:K02F3.11

A/Experimental source: strain Bristol N2

C/Genetics:

A/Genes: CESP:K02F3.11

A/introns: 257/2

Query Match 90.9%; Score 60; DB 2; Length 304;  
Best Local Similarity 93.3%; Pred. No. 0.98;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSG 15

DB 14 SSSSSSSSSSSSSSG 28

##### RESULT 2

T26294

hypothetical protein W09C2.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 16-Aug-2000

C/Accession: T26294

R/Lloyd, C.

submitted to the EMBL Data Library, December 1995

A/Reference number: Z20191

A/Accession: T26294

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1249 <WIL>

A/Cross-references: EMBL:Z68221; PIDN:CAA92495.1; GSPDB:GN00022; CESP:W09C2.3

A/Experimental source: clone W09C2

C/Genetics:

A/Genes: CESP:W09C2.3

A/Map position: 4

A/introns: 32/3; 58/3; 117/3; 211/3; 263/3; 675/3; 1139/3; 1187/1; 1230/3

C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain <ATN>

Query Match 86.4%; Score 57; DB 2; Length 1249;

A/Reference number: 538158

```
A:Accession: S38170
A:Molecule type: DNA
A:Residues: 1-406 <BAL>
A:Cross-references: UNIPROT:P32583; EMBL:Z28317; NID:g486560; PID:g486581; MIPS:YKR092c
A:Experimental source: strain S288C
R:Bou, G.; Batean, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, M.; Ji
Yeast 9, 1349-1354, 1993
A>Title: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae chromo
A:Reference number: S40644; MUID:94205265; PMID:8154186
A:Accession: S40645
A:Molecule type: DNA
A:Residues: 1-406 <BOU>
A:Cross-references: EMBL:X73541; NID:g450550; PIDN:CAA51946.1; PID:g450552
A:Experimental source: strain S288C
R:Laio, D.; Carles, C.; Sentenac, A.; Thuriaux, P.
Submitted to the EMBL Data Library, May 1993
A:Description: Interactions between three common subunits of yeast RNA polymerases I and
A:Reference number: S37702
A:Accession: S37702
A:Molecule type: DNA
A:Residues: 1-399,'N',401-406 <LAL>
A:Cross-references: EMBL:L1275; NID:g295670; PID:g295671
A:Genetic:
A:Gene: SGD:SRP40
A:Cross-references: SGD:S0001800; MIPS:YKR092c
A:Map position: 11R

Query Match      81.8%  Score 54;  DB 2;  Length 406;
Best Local Similarity 92.9%  Pred. No. 6.9;
Matches 13;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Oy      1 SSSGSSSSSSSSSS 14
Db      100 SSSGSSSSSSSSSS 113

RESULT 8
T08093
oleosin homolog STA 41-2 - rape
C:Species: Brassica napus (rape)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
A:Accession: T08093
R:Robert, L.S.; Gerster, J.; Allard, S.; Cass, L.; Simmonds, J.
Plant J. 6, 927-933, 1994
A>Title: Molecular characterization of two Brassica napus genes related to oleosins whic
A:Reference number: Z16348; MUID:95152562; PMID:7849761
A:Accession: T08093
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-424 <ROB>
A:Cross-references: UNIPROT:Q42626; EMBL:I33282; NID:g495010; PIDN:AAA70400.1; PID:g9042
A:Experimental source: cv. Westar; tapetum
A>Note: protein component of lipid storage bodies of plants
C:Genetic:
A:Geno: STA 41-2

Query Match      81.8%  Score 54;  DB 2;  Length 424;
Best Local Similarity 80.0%  Pred. No. 7.2;
Matches 12;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Oy      1 SSSGSSSSSSSSSSG 15
Db      400 SSSGSSSSSDGSSSDG 414

RESULT 9
S49886
probable membrane protein YII123w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein Y18277.06
C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
A:Accession: S49886
R:Hamlyn, N.; Churcher, C.
```

```
submitted to the EMBL Data Library, November 1994
A:Reference number: S49881
A:Accession: S49886
A:Molecule type: DNA
A:Residues: 1-475 <HAN>
A:Cross-references: UNIPROT:P40472; GB:Z47047; EMBL:Z46833; NID:g603997; PID:g763223; MI
C:Genetic:
A:Gene: SGD:SIM1
A:Cross-references: SGD:S0001385; MIPS:YII123w
A:Map position: 9L
C:Superfamily: Saccharomyces NCA3 protein
C:Keywords: transmembrane protein
F:82-98/Domain: transmembrane #status predicted <TM>

Query Match      81.8%  Score 54;  DB 2;  Length 475;
Best Local Similarity 86.7%  Pred. No. 8;
Matches 13;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

Oy      1 SSSGSSSSSSSSSSG 15
Db      186 SSSGSSSSSSSSSSG 200

RESULT 10
S33167
gene pointed protein splice form 1 - fruit fly (Drosophila melanogaster)
N:Alternate names: ETS-like protein
C:Species: Drosophila melanogaster
C:Date: 13-Jan-1995 #sequence_revision 30-May-1997 #text_change 09-Jul-2004
A:Accession: S33167; S28819; S28818
R:Klaemdt, C.
Development 117, 163-176, 1993
A>Title: The Drosophila gene pointed encodes two ETS-like proteins which are involved in
A:Reference number: S33167; MUID:94038653; PMID:823245
A:Accession: S33167
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-623 <KLA>
A:Cross-references: UNIPROT:P51022; EMBL:X69166; NID:g288079; PIDN:CAA48916.1; PID:g28808
R:Chen, T.; Bunting, M.; Karim, F.D.; Thummel, C.S.
Dev. Biol. 151, 176-191, 1992
A>Title: Isolation and characterization of five Drosophila genes that encode an ets-relat
A:Reference number: S28819; MUID:92249640; PMID:1577186
A:Accession: S28819
A:Molecule type: mRNA
A:Residues: 456-613 <CHE>
A:Cross-references: EMBL:M88472; NID:g157191; PIDN:AAC34200.1; PID:g157192
R:Pirbyl, L.J.; Watson, D.K.; McWilliams, M.J.; Ascione, R.; Papas, T.S.
Dev. Biol. 127, 45-53, 1988
A>Title: The Drosophila ets-2 gene: molecular structure, chromosomal localization, and de
A:Reference number: S28818; MUID:88196618; PMID:2834248
A:Accession: S28818
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 445-466,'R',468-603 <PRI>
A:Cross-references: EMBL:M20408; NID:g157384; PIDN:AAA28521.1; PID:g157385
A>Note: the authors translated the codon AGA for residue 467 as Gln
C:Genetic:
A:Gene: FlyBase:put
A:Cross-references: FlyBase:FBgn0003118
A:Introns: 550/3
C:Superfamily: pointed protein, splice form 1; ets DNA-binding domain homology
C:Keywords: alternative splicing; DNA binding; nucleus; transcription factor
F:517-595/Domain: ets DNA-binding domain homology <BTS>

Query Match      81.8%  Score 54;  DB 1;  Length 623;
Best Local Similarity 85.7%  Pred. No. 10;
Matches 12;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;

Oy      1 SSSGSSSSSSSSSSS 14
Db      158 TTSSGSSSSSSSSSSS 171
```

RESULT 11  
AC0333  
Probable membrane protein YP02731 [imported] - Yersinia pestis (strain CO92)  
C/Species: Yersinia pestis  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C/Accession: AC0333  
R/Parkhill, J.; Wen, B.W.; Thomson, N.R.; Tiltball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, N.  
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A/Reference number: AB0001; MUID:21470413; PMID:11586360  
A/Accession: AC0333  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-679 <KIR>  
A/Cross-references: UNIPROT:Q8ZD61; GB:AL590842; PIDN:CAC92970.1; PID:G15980709; GSPDB:C/Gene: YP02731

Query Match 81.8%; Score 54; DB 2; Length 679;  
Best Local Similarity 80.0%; Pred. No. 11;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 SSSSGSSSSSSSSSG 15  
Db 654 SSSSGSSSSSSSSSG 668

RESULT 12  
152882  
antigen - human  
C/Species: Homo sapiens (man)  
C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: 152882  
R/Bloch, D.B.; Rabkina, D.; Quertermous, T.; Bloch, K.D.  
Clin. Immunol. Immunopathol. 72, 380-389, 1994  
A/Title: The immunoreactive region in a novel autotigen contains a nuclear localization  
A/Reference number: 152882; MUID:94340813; PMID:750377  
A/Accession: 152882  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-1215 <RES>  
A/Cross-references: UNIPROT:Q13826; GB:L26339; NID:G533201; PIDN:AAA21833.1; PID:G533202  
C/Superfamily: human autotigen Ge-1

Query Match 81.8%; Score 54; DB 2; Length 1215;  
Best Local Similarity 92.9%; Pred. No. 19;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 SSSSGSSSSSSSSSG 14  
Db 614 SSSSGSSSSSSSSSG 627

RESULT 13  
T02345  
hypothetical protein KIAA0324 - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C/Accession: T02345  
R/Ricke, D.O.; Bruce, D.; Muntz, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, D.; re, J.; White, S.; Ueng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L.  
submitted to the EMBL Data Library, March 1998  
A/Description: Sequencing of human chromosome 16p13.3.  
A/Reference number: Z14664  
A/Accession: T02345  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1791 <RIC>  
A/Cross-references: UNIPROT:O60382; EMBL:AC004493; NID:G2996648; PIDN:AAC08453.1; PID:G2  
C/Genetics:

A/Map position: 16  
A/Introns: 1610/2; 1706/2  
A/Note: KIAA0324

Query Match 81.8%; Score 54; DB 2; Length 1791;  
Best Local Similarity 86.7%; Pred. No. 28;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 SSSSGSSSSSSSSSG 15  
Db 1575 SSSSGSSSSSSSSSG 1589

RESULT 14  
T29088  
vitellogenin I precursor [validated] - chicken  
N/Contents: lipovitellin I; lipovitellin II; phosvitin; yolk glycoprotein 42K  
C/Species: Gallus gallus (chicken)  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T29088; S55681  
R/Mabuchi, N.; Yamamura, J.; Adachi, T.; Aoki, N.; Nakamura, R.; Matsuda, T.  
submitted to the EMBL Data Library, November 1996  
A/Description: cDNA cloning and estrogen-induced expression of chicken vitellogenin I.  
A/Reference number: Z20557  
A/Accession: T29088  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-1912 <MAB>  
A/Cross-references: UNIPROT:P87498; EMBL:D89547; PIDN:BAAL3973.1  
A/Experimental source: liver  
R/Yamamura, J.; Adachi, T.; Aoki, N.; Nakajima, H.; Nakamura, R.; Matsuda, T.  
Biochem. Biophys. Acta 1244, 384-394, 1995  
A/Title: Precursor-product relationship between chicken vitellogenin and the yolk protein

A/Reference number: S55680; MUID:95322425; PMID:7599159  
A/Accession: S55681  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1628-1639 <YAM>  
C/Superfamily: vitellogenin  
C/Keywords: egg yolk; glycoprotein; liver; phosphoprotein  
F/1-15/Domain: signal sequence #status predicted <SIG>  
F/16-1912/Product: vitellogenin I #status predicted <MAB>

Query Match 81.8%; Score 54; DB 2; Length 1912;  
Best Local Similarity 92.9%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 SSSSGSSSSSSSSSG 14  
Db 1150 SSSSGSSSSSSSSSG 1163

RESULT 15  
A35419  
neutrophil protein - pig (fragment)  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 09-Jul-2004  
C/Accession: A35419  
R/Bellavite, P.; Bazzoni, F.; Cassatella, M.A.; Hunter, K.J.; Bannister, J.V.  
Biochem. Biophys. Res. Commun. 170, 915-922, 1990  
A/Title: Isolation and characterization of a cDNA clone for a novel serine-rich neutrophil  
A/Reference number: A35419; MUID:90345818; PMID:1656479  
A/Accession: A35419  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-284 <BEL>  
A/Cross-references: UNIPROT:Q99311; GB:M55701; NID:G164672; PIDN:AAA63449.1; PID:G164673

Query Match 78.8%; Score 52; DB 2; Length 284;  
Best Local Similarity 86.7%; Pred. No. 8.6;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 SSSSSSSSSSSSSSG 15  
| | | | |  
Db 146 SSSSSSSSTSSSG 160

Search completed: April 4, 2005, 15:58:06  
Job time : 6.41534 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 25.3514 seconds  
(without alignments)  
302.988 Million cell updates/sec

Title: US-09-887-853-8  
Perfect score: 66  
Sequence: 1 SSSSSSSSSSSSSSG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	192	2	Q7YY80 cryptospori
2	66	100.0	289	2	Q21155 caenorhabd
3	66	100.0	453	2	Q6C6N1 Q6cen1 yarrowia 11
4	60	90.9	368	2	Q6WNT4 fugu rubrip
5	60	90.9	1357	2	Q9W4M4 drosophila
6	59	89.4	218	2	Q759N0
7	59	89.4	619	2	Q7PQ47 ashbya goes
8	58	87.9	394	2	Q8T010 anopheles g
9	58	87.9	525	2	Q693B7 microbubif
10	58	87.9	1124	2	Q7QDA9 anopheles g
11	57	86.4	300	2	Q86JX6 dictyostel
12	57	86.4	303	2	Q95VT3
13	57	86.4	419	2	Q9W9E1 drosophila
14	57	86.4	694	2	Q9CS92 mus musculi
15	57	86.4	1228	2	Q45215 caenorhabd
16	57	86.4	1249	2	Q6T363 caenorhabd
17	57	86.4	1352	2	Q6T364 caenorhabd
18	57	86.4	1388	2	Q69363 caenorhabd
19	57	86.4	1403	2	Q9VPO4
20	57	86.4	1488	2	Q86B57 drosophila
21	57	86.4	1751	2	Q26194 plameodim
22	56	84.8	367	2	Q86KL5 dictyostel
23	56	84.8	400	1	RTOA_DICDI
24	56	84.8	477	2	Q9FCW9 arabidopsi
25	56	84.8	544	2	Q54802 mus musculi
26	56	84.8	544	2	Q794H2 mus sp. md2
27	56	84.8	590	2	Q693B6 microbubif
28	56	84.8	683	2	Q9PDW2 xylella fas
29	56	84.8	773	2	P79149 canis fami
30	55	83.3	283	2	Q6NZV7 brachydanio
31	55	83.3	283	2	Q6PG31 brachydanio

32	55	83.3	332	2	Q6C1Z7 yarrowia 11
33	55	83.3	410	2	Q7S340 neurospora
34	54	81.8	69	2	Q863P8 dictyostel
35	54	81.8	90	2	Q7RWL2 neurospora
36	54	81.8	107	2	Q9M0B5 arabidopsi
37	54	81.8	149	2	Q8CSW6 mus musculi
38	54	81.8	162	2	Q6BD40 drosophila
39	54	81.8	162	2	Q9M0B4 arabidopsi
40	54	81.8	167	2	Q6EP11 oryza sativ
41	54	81.8	202	2	Q9V760 drosophila
42	54	81.8	203	2	Q8WMA1 homo sapien
43	54	81.8	203	2	Q9NUZ4 homo sapien
44	54	81.8	256	2	Q82F25 streptomyce
45	54	81.8	266	2	Q9H0J0 homo sapien

## ALIGNMENTS

RESULT 1  
Q7YY80 PRELIMINARY; PRT; 192 AA.  
AC Q7YY80;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Serine repeat antigen, probable.  
GN ORFNames=56k.04;  
OS Cryptosporidium parvum.  
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
OC Cryptosporidiidae; Cryptosporidium.  
OX NCBI\_TaxID=5807;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Banker A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M.,  
RA Vogel C., Teichmann S.A., Ivens A., Dear P.H.;  
RT Integrated mapping, chromosomal sequencing and sequence analysis of  
RT Cryptosporidium parvum.  
RL Genome Res. 0:0-0(2003).  
DR EMBL; BX538350; CAD98606.1; .  
SQ SEQUENCE 192 AA; 19686 MW; CB363BP9B40F77 CRC64;

Query Match 100.0%; Score 66; DB 2; Length 192;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSSSSSSSSSSSSSG 15  
DB 155 SSSSSSSSSSSSSSG 169  
(1)

RESULT 2  
Q21155 PRELIMINARY; PRT; 289 AA.  
AC Q21155;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Rnp (Rnm rna binding domain) containing protein 5.  
GN Name-rnp-5; ORFNames=K02F3.11;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA STRAIN-Bristol NZ;  
RC MEDLINE=9069613; PubMed=9851916;  
RG Wormbase Consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for  
RT investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018 (1998).  
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RT "The sequence of C. elegans cosmid K02F3."
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U00052; AKK21429.2; -.
DR WormBase; WBGene00004388; rmp-5.
DR WormFep; K02F3.11; CE2981.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF00076; RRM_1; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 289 AA; 3237 MW; CFE82B8BD2E230E CRC64;

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Query Match          100.0%; Score 66; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SSSSSSSSSSSSSSG 15
DB 19 SSSSSSSSSSSSSSG 33

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RESULT 3
OC6CN1 PRELIMINARY; PRT; 453 AA.
AC OC6CN1;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DB Similar to tr|008294 Saccharomyces cerevisiae Y01J55C.
GN ORFNames=YAL10S080089;
OS Yarrowia lipolytica C11B99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SBOUNCE FROM N.A.
RC STRAIN=C11B99;
RG Genolevures;
RA Lafontaine I., de Montigny J., Marck C., Neugegliste C., Talla B.,
RA Goffard N., Frangoul L., Aigle M., Anthonard V., Babor A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boistrane A., Boyer J., Cactolico L., Contandololet F., de Darivar A.,
RA Despons L., Fabre E., Falthead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hemequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozler-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof B., Wilth B.,
RA Zenlou-Meyer M., Zivanovic I., Boliotin-Fukuhara M., Thierry A.,

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RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in Yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C11B99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382131; CAG79270.1; -.
SQ SEQUENCE 453 AA; 43707 MW; 097090FA7AE15F50 CRC64;

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Query Match          100.0%; Score 66; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SSSSSSSSSSSSSSG 15
DB 341 SSSSSSSSSSSSSSG 355

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RESULT 4
OC6NNT4 PRELIMINARY; PRT; 368 AA.
AC OC6NNT4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DR 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Transcription factor Sox11.
GN Name=Sox11;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=15019997; DOI=10.1016/j.gene.2003.12.008;
RA Koopman P., Schepers G., Brenner S., Venkatesh B.;
RT "Origin and diversity of the SOX transcription factor gene family:
RT genome-wide analysis in Fugu rubripes.";
RL Gene 328:177-186(2004).
DR EMBL; AY277959; AA018502.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR009071; HMG-box.
DR InterPro; IPR000910; HMG-box.
DR Pfam; PF00505; HMG_box; 1.
DR SMART; SM00398; HMG; 1.
DR PROSITE; PS50118; HMG_BOX_2; 1.
SQ SEQUENCE 368 AA; 40719 MW; ECF681E0D74EFD7 CRC64;

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Query Match          90.9%; Score 60; DB 2; Length 368;
Best Local Similarity 93.3%; Pred. No. 6.8;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 SSSSSSSSSSSSSSG 15
DB 272 SSSSSSSSSSSSSSG 286

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RESULT 5
OC9W4M4 PRELIMINARY; PRT; 1357 AA.
AC OC9W4M4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CG15570-PA.
GN ORFNames=CG15570;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCB1\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abril J.F., Abmayr A., An H.J., Andrews-Pfankuch C., Baldwin D.,  
 RA Bailev R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boltshakov S.,  
 RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,  
 RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ipeegwan C.,  
 RA Jajuli M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lei Z.,  
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mlehnina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puti V., Reese M.G.,  
 RA Rehnert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spletter E., Sprelding A.C., Stapleton M., Strong R., Sun E.,  
 RA Svetskaia R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wasearan D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodgett W., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RL "The genome sequence of *Drosophila melanogaster*.";   
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=24246065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Krommler B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Friese E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svetskaia R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RL "Finishing a whole-genome ehoicun: Release 3 of the *Drosophila*  
 RL melanogaster euchromatic genome sequence.";   
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=24246070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Krommler B., Carlson J., Svetskaia R.,  
 RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RL "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RL a genomics perspective.";   
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=24246069; PubMed=12537572;  
 RA Miya S., Croby M.A., Mungall C.U., Mathews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RL "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review.";   
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX PLAYBASE (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX PLAYBASE (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE004330; AAF45927.1; --  
 DR Flybase: FBgn0029697; CG15570.  
 SQ SEQUENCE 1357 AA; 136890 MW; C282DC86FE34A61A CRC64;  
 Query Match 90.9%; Score 60; DB 2; Length 1357;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSSSSSSSSSSSSS 14  
 DB 563 SSSSSSSSSSSSSS 576  
 RESULT 6  
 ID Q759N0 PRELIMINARY; PRT; 218 AA.  
 AC Q759N0;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE ADR246CD.  
 GN ORFNames=ADR246C;  
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetalea; Saccharomycetaceae; Eremothecium.  
 NC NCB1\_TaxId=33169;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 10895;  
 RA Voegelé S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,  
 RA Philpott P.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE016817; AAS52166.1; --  
 DR AGD; ADR246C; --  
 SQ SEQUENCE 218 AA; 19346 MW; 7B5103F9D1B0BC52 CRC64;  
 Query Match 89.4%; Score 59; DB 2; Length 218;  
 Best Local Similarity 86.7%; Pred. No. 5.1;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SSSSSSSSSSSSSG 15  
 DB 167 SSSSSSSSTGSSGSG 181  
 RESULT 7  
 Q7P047 PRELIMINARY; PRT; 619 AA.  
 AC Q7P047;  
 DT 01-MAR-2004 (TREMBLrel. 26, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE ENSANGP0000021699 (Fragment).  
 GN Name=ENSANGG00000019210.  
 OS Anopheles gambiae str. PE8T.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Anophelinae;  
 NC NCB1\_TaxId=180454;  
 RN [1]  
 RP SEQUENCE FROM N.A.

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RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008900; EAA09315.2; -.
FT NON_TER 1 1
FT NON_TER 619 619
SQ SEQUENCE 619 AA; 60241 MW; 3A74385560D44E93 CRC64;

Query Match
Best Local Similarity 89.4%; Score 59; DB 2; Length 619;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSSGSSSSSSSSSG 15
DB 222 SSSGSSSSSSSSSG 236

RESULT 8
O8T0L0 PRELIMINARY; PRT; 394 AA.
ID O8T0L0
AC O8T0L0;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Hypothetical protein MA1742.
GN OrderedlocusNames=MA1742;
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., MacDonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Alnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearlilano K., Johnson R.,
RA Lincon L., McEwan P., McKernan K., Talama J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umyam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.D., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AEO10848; AAM05149.1; -.
DR InterPro; IPR008962; Papd-like.
KW Complete proteome.
SQ SEQUENCE 394 AA; 42431 MW; 1D2C7304B147D6B CRC64;

Query Match
Best Local Similarity 87.9%; Score 58; DB 2; Length 394;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSSGSSSSSSSSSG 15
DB 132 SSSGSSSSSSSG 145

RESULT 9
O693B7 PRELIMINARY; PRT; 525 AA.
ID O693B7;
AC O693B7;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Endo-chitinase.

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GN Name=chIB;
OS Microbubifer hydrolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Microbubifer.
OX NCBI_TaxID=48074;
RN [1]
RP SEQUENCE FROM N.A.
RA Howard M.B., Ekborg N.A., Taylor L.E. Jr., Weiner R.M.,
RA Hutcheson S.W.;
RT "Complex polyaccharide metabolic profiles of Microbubifer sp. and
RT analysis of chitinases and other degradative enzymes of Microbubifer
RT hydrolyticus.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY646087; AAT01213.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0030246; C:carbohydrate binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004553; F:hydrolase activity; hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR003610; CEM_5_12.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF02839; CEM_5_12; 2.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR SMART; SM00495; ChbD3; 2.
DR PROSITE; PS01095; CHITINASE_18; UNKNOWN_1.
KW Glycosidase; Hydrolyase.
SQ SEQUENCE 525 AA; 53761 MW; 3794374935464EA9 CRC64;

Query Match
Best Local Similarity 87.9%; Score 58; DB 2; Length 525;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSSGSSSSSSSSSG 15
DB 192 SSSGSSSSSSSG 206

RESULT 10
O70DA9 PRELIMINARY; PRT; 1124 AA.
ID O70DA9
AC O70DA9;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE AgCP1543.
GN Name=agCG55963; ORFNames=ENSNANG0000015740;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008859; EAA07880.1; -.
DR InterPro; IPR002553; Adaptin_N.
DR InterPro; IPR008938; ARM.
DR Pfam; PF01602; Adaptin_N; 1.
SQ SEQUENCE 1124 AA; 122427 MW; 06332B0FCB5AD1F4 CRC64;

Query Match
Best Local Similarity 87.9%; Score 58; DB 2; Length 1124;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSSGSSSSSSSSSG 15
DB 736 SSSGSSSSSSSG 749

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RESULT	11
ID	Q86UX6
AC	Q86UX6; PRELIMINARY;
DT	01-JUN-2003 (TREMBLrel. 24, Created)
D7	01-JUN-2003 (TREMBlrel. 24, Last sequence update)
D7	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	Similar to Dictyostelium discoideum (Slime mold). CF50.
OS	Dictyostelium discoideum (Slime mold).
OC	Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX	NCBI_TaxID=44689;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=AX4;
RX	MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA	Gloechner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA	Lehmman R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA	Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RL	"Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
RM	[2]
RN	SEQUENCE FROM N.A.
RC	STRAIN=AX4;
RA	Baumgart C.;
DR	EMBL; AC116984; AAC51376.1; -
DR	DictyBase; DDB0185090; CF50.
DR	GO; GO:0003796; F:lysozyme activity; IEA.
DR	GO; GO:0016998; P:cell wall catabolism; IEA.
DR	GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR	InterPro; IPR002053; Glyco_hydro_25.
DR	Prodont; PD004620; Glyco_hydro_25.1.
SO	SEQUENCE 300 AA; 30480 MW; FAFFBS7AD967467 CRC64;
Query Match	Best Local Similarity 86.4%; Score 57; DB 2; Length 300;
Matches	12; Conservative 3; Mismatches 0; Indels 0; Gaps 0,
QY	1 SSSSGSSSGSSSGS 15    :::  :    :
Db	254 SSNSGSSNSGSSNG 268
RESULT	12
ID	Q95VT3
AC	Q95VT3; PRELIMINARY;
PRT	303 AA.
DT	01-DEC-2001 (TREMBLrel. 19, Created)
D7	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	CF50.
GN	Name=cfs0;
OS	Dictyostelium discoideum (Slime mold).
OC	Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX	NCBI_TaxID=44689;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=2211679; Pubmed=12117815;
RA	Brock D.A., Hutton R.D., Giurgutiu D.V., Scott B., Ammann R.,
RA	Gomer R.H.;
RT	"The different components of a multiaunit cell number-counting factor have both unique and overlapping functions.";
RL	Development 129:1657-1668(2002).
DR	EMBL; AF405695; AL01036.1; -
DR	DictyBase; DDB0185090; CF50.
SO	SEQUENCE 303 AA; 30854 MW; 2B2A3CC1CEE3CEBA CRC64;
Query Match	Best Local Similarity 86.4%; Score 57; DB 2; Length 303;
Matches	12; Conservative 3; Mismatches 0; Indels 0; Gaps 0,

Oy	1	SSSSGSSSSGSSG 15
Db	257	SSSSGSSSSGSSNG 271
RESULT 13		
Q9WM91	PRELIMINARY;	PTI; 419 AA.
Q9WM91	Q8YTE6;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)	
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)	
DE	CG7290-PA (REF5123p) .	
CN	ORFNames=CG7290;	
OS	Drosophila melanogaster (Fruit fly) .	
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydroidea; Drosophilidae; Drosophila.	
OX	NCBI_TaxId=7227;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;	
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,	
RA	Amannikides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	
RA	Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,	
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,	
RA	Abriell J.F., Aghayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,	
RA	Balcer R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	
RA	Beeson K.Y., Benos P.V., Bermale B.P., Bhandari D., Bolshakov S.,	
RA	Botkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,	
RA	Buttles K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	
RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	
RA	Feiler C., Gabriellian A.E., Gang N.S., Gelbart W.M., Glaeser K.,	
RA	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,	
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.H., Ibeagwam C.,	
RA	Jatalai M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	
RA	Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,	
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,	
RA	Nelson D.R., Nelson K.A., Nixon K., Nussearn D.R., Paley J.M.,	
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,	
RA	Reinert K., Remington K., Saunders R.D., Scheefel F., Shen H.,	
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,	
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,	
RA	Syrkbas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	
RA	Wang Z.Y., Wasserman D.A., Weinstock G.M., Weisenbach J.,	
RA	Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,	
RA	Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C. ;	
RT	"the genome sequence of Drosophila melanogaster." ;	
RL	Science 287;2185-2195(2000) .	
RL	[2]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=22426065; PubMed=12537568;	
RA	Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,	
RA	Geisel S., Adams M., Champe M., Dugan S.P., Fries E., Hoggson A.,	
RA	George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,	
RA	Paley J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,	
RA	Syrkbas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,	
RA	Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,	
RT	"finishing a whole-genome shotgun. Release 3 of the Drosophila	
RL	melanogaster euchromatic genome sequence " ;	
RL	Genome Biol 3;RESEARCH0079-RESEARCH0079(2002) .	
RL	[3]	

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RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminler J.S., Bergman C.M., Krommiller B., Carlson J., Swirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celinker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Mitra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu I., Berman B.P.,
RA Bellencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Lao G.,
RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celinker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RX EMBL; AEO03514; AAF49058.3; -
EMBL; AY071600; AAL49222.1; -
DR InChit; O9VM91; -
DR FlyBase; FBgn0036949; CG7290.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR Pfam; PF01607; CBM_14; 5.
DR SMART; SM00494; ChtBD2; 5.
DR PROSITE; PS50940; CHIT_BIND_II; 5.
DR SEQUENCE 419 AA; 42406 MW; DE8E397DD009DF2 CRC64;
SQ

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Query Match 86.4%; Score 57; DB 2; Length 419;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SSSSSSSSSSSSSSSG 15
Db 351 TSSSSSSTSSGSGTSSG 365

RESULT 14
Q9CS92 PRELIMINARY; PRT; 694 AA.
AC Q9CS92;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-MAR-2004 (TEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:5730406M06 product:hypothetical Serine-rich region
DE containing protein, full insert sequence. (Fragment).
GN Name=5730406M06Rik;
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Riken Genome Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium;
RA "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro T., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Warahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi U., Aizawa K., Akahira S., Akimura T., Arai A., Kono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imocani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Tejima Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RX EMBL; AK017507; BAB30779.2; -
DR MGD; MGI:1913875; 5730406M06Rik.
KW Hypothetical protein.
FT NON TER 694
SQ SEQUENCE 694 AA; 79382 MW; 699D6A63F6A07D0D CRC64;

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Query Match 86.4%; Score 57; DB 2; Length 694;
Best Local Similarity 92.9%; Pred. No. 31;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2 SSSGSSSSGSSSG 15  
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 Db 508 BRGSSSSGSSSG 521

## RESULT 15

ID 045215 PRELIMINARY; PRT; 1228 AA.  
 AC 045215;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)  
 DE Calcium ATPase.  
 GN Name=mca-1; ORFNames=M09C2.3;  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pelodertinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CB1489 him-8;  
 RX MEDLINE=99134356; PubMed=9933625; DOI=10.1074/jbc.274.7.4254;  
 RA Kraev A., Kraev N., Carafoli E.;  
 RT "Identification and functional expression of the plasma membrane  
 calcium ATPase gene family from Caenorhabditis elegans.";  
 RL J. Biol. Chem. 274:4254-4258(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CB1489 him-8;  
 RA Kraev A.S.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ223616; CAU1491.1; -  
 DR GO: GO:0016021; C: integral to membrane; IEA.  
 DR GO: GO:0005524; F: ATP binding; IEA.  
 DR GO: GO:0005509; F: calcium ion binding; IEA.  
 DR GO: GO:0005388; F: calcium-transporting ATPase activity; IEA.  
 DR GO: GO:0016787; F: hydrolase activity; IEA.  
 DR GO: GO:0016820; F: hydrolase activity, acting on acid anhydrid. . .; IEA.  
 DR GO: GO:0006816; F: calcium ion transport; IEA.  
 DR GO: GO:0006812; F: calcium transport; IEA.  
 DR GO: GO:0008152; P: metabolism; IEA.  
 DR InterPro: IPR006408; ATPase-IB Ca.  
 DR InterPro: IPR001757; ATPase\_EI-E2.  
 DR InterPro: IPR006068; Cation\_ATPase\_C.  
 DR InterPro: IPR004014; Cation\_ATPase\_N.  
 DR InterPro: IPR005834; Dehal\_like\_hydro.  
 DR Pfam: PF00689; Cation\_ATPase\_C; 1.  
 DR Pfam: PF00690; Cation\_ATPase\_N; 1.  
 DR Pfam: PF00122; EI-E2\_ATPase; 1.  
 DR Pfam: PF00702; Hydrolase; 1.  
 DR PRINTS: PR00119; CATATPASE.  
 DR TIGRFAMs: TIGR01517; ATPase-IB Ca; 1.  
 DR TIGRFAMs: TIGR01494; ATPase\_P-type; 3.  
 DR PROSITE: PS00154; ATPASE\_EI-E2; UNKNOWN 1.  
 SQ SEQUENCE 1228 AA; 134552 MW; 1F790DFEBBA6108 CRC64;

QY 1 SSSGSSSSGSSSG 15  
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 Db 314 SSSSSSSGSSSG 328

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 Job time : 27.3514 secs

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